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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:25:20 ; Search time 32 Seconds

(without alignments)
327.502 Million cell updates/sec

Title: US-09-869-566-5

Perfect score: 1059
Sequence: 1 MSALLILALVGAIVADYKDD.....IEFSFQVCKAKMSPEVSD 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTCUTS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895	84.5	218	4	US-09-293-625-2
2	895	84.5	218	4	US-09-398-412B-4
3	863.5	81.5	218	4	US-09-398-412B-2
4	702	66.3	167	3	US-09-128-155-7
5	702	66.3	178	3	US-09-128-155-2
6	695	65.6	136	3	US-09-128-155-11
7	623	58.8	115	3	US-09-128-155-5
8	623	58.8	115	3	US-09-128-155-9
9	623	58.8	115	3	US-09-128-155-13
10	473.5	44.7	185	3	US-09-128-155-18
11	229.5	21.7	169	2	US-08-790-032-2
12	229.5	21.7	169	3	US-09-069-619-2
13	229.5	21.7	169	4	US-09-494-018-2
14	229.5	21.7	169	4	US-09-398-412B-15
15	191.5	18.1	156	4	US-09-398-412B-13
16	174.5	16.5	155	3	US-09-417-455-5
17	174.5	16.5	155	4	US-09-348-942-5
18	174.5	16.5	155	4	US-09-316-081-5
19	174.5	16.5	155	4	US-09-578-458-5
20	174.5	16.5	155	4	US-09-523-964A-5
21	174.5	16.5	155	4	US-09-457-626-5
22	174.5	16.5	155	4	US-09-576-008-5
23	171	16.1	160	4	US-09-398-412B-14
24	167	15.8	178	3	US-09-000-630C-21
25	167	15.8	178	3	US-08-862-730C-21
26	167	15.8	178	3	US-09-417-455-9
27	167	15.8	178	4	US-09-348-942-9

28	167	15.8	178	4	US-09-457-626-9	Sequence 9, Appli
29	167	15.8	178	4	US-09-576-008-9	Sequence 9, Appli
30	165.5	15.6	152	4	US-08-476-860-18	Sequence 18, Appli
31	161	15.2	180	1	US-08-910-733-13	Sequence 13, Appli
32	161	15.2	180	2	US-08-910-884-13	Sequence 13, Appli
33	161	15.2	180	2	US-08-459-811-2	Sequence 2, Appli
34	158.5	15.0	159	1	US-08-484-598-2	Sequence 2, Appli
35	158.5	15.0	159	2	US-08-459-092-2	Sequence 2, Appli
36	158.5	15.0	159	2	US-08-459-814-2	Sequence 2, Appli
37	158.5	15.0	159	2	US-08-425-232-2	Sequence 2, Appli
38	158.5	15.0	159	2	US-08-471-227-3	Sequence 3, Appli
39	158.5	15.0	159	2	US-08-479-140-2	Sequence 2, Appli
40	158.5	15.0	159	2	US-08-477-143-2	Sequence 2, Appli
41	158.5	15.0	159	3	US-09-417-455-14	Sequence 14, Appli
42	158.5	15.0	159	4	US-09-348-942-14	Sequence 14, Appli
43	158.5	15.0	159	4	US-09-316-081-9	Sequence 9, Appli
44	158.5	15.0	159	4	US-09-578-458-9	Sequence 9, Appli
45	158.5	15.0	159	4	US-09-578-458-9	Sequence 9, Appli

ALIGNMENTS

```
RESULT 1
US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293,625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-625-2

Query Match      84.5%  Score 895;  DB 4;  Length 218;
Best Local Similarity 100.0%;  Pred. No. 9.4e-97;
Matches 169;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      35 PKVKNLPKPKSHDQDKVVLDSGNLIAPDKNYIRPEIFALASSLSASAEKSGPI 94
      |||
DB      50 PKVKNLPKPKSHDQDKVVLDSGNLIAPDKNYIRPEIFALASSLSASAEKSGPI 109
      |||
QY      95 LLSVSKBEFCLYCDKDGQSHPSLQLKKEKLMKLAOKESARRPPIFYRAOVGSWMML 154
      |||
DB      110 LLSVSKBEFCLYCDKDGQSHPSLQLKKEKLMKLAOKESARRPPIFYRAOVGSWMML 169
      |||
QY      155 AAHGMWFTCSNCPNPGVTDKFKENRKHIEFSFQVCKAKMSPEVSD 203
      |||
DB      170 AAHGMWFTCSNCPNPGVTDKFKENRKHIEFSFQVCKAKMSPEVSD 218
      |||

RESULT 2
US-09-398-412B-4
; Sequence 4, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
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SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-09-398-412B-4

Query Match
Best Local Similarity 100.0%; Pred. No. 9.4e-97; Length 218;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVKNILPKKFSIHDDHKLVLVDSGNLIAVPDKNYIRPEIFALASSLSASAEKGSPT 94
DB 50 PKVKNILPKKFSIHDDHKLVLVDSGNLIAVPDKNYIRPEIFALASSLSASAEKGSPT 109
QY 95 LIGVSKGEFLCYCDKXGSHPSLQKKEKMLKLAOKESARRPIFYRAQVGSNMWLES 154
DB 110 LIGVSKGEFLCYCDKXGSHPSLQKKEKMLKLAOKESARRPIFYRAQVGSNMWLES 169
QY 155 AAHGWFICTSCNCPNPEVGTDKFENRKHIEFSFQVCKAEKMSPEVSD 203
DB 170 AAHGWFICTSCNCPNPEVGTDKFENRKHIEFSFQVCKAEKMSPEVSD 218

RESULT 3
US-09-398-412B-2
Sequence 2, Application US/09398412B
Patent No. 6680380
GENERAL INFORMATION:
APPLICANT: Tiansu, Jacqueline C.
TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
FILE REFERENCE: DX0904K
CURRENT APPLICATION NUMBER: US/09/398,412B
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US 60/100948
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-09-398-412B-2

Query Match
Best Local Similarity 81.5%; Score 863.5; DB 4; Length 218;
Matches 172; Conservative 5; Mismatches 11; Indels 15; Gaps 2;

QY 16 DYKDDDDKLA---AANSALCRGP-----KVNINPKKFSIHDDHKLVLVDSG 60
DB 16 DWEKDEPQCCLLEDPAGSPLEPGSLPTMNFVHSRKYSINPKKFSIHDDHKLVLVDSG 75
QY 61 NLIAVPDKNYIRPEIFALASSLSASAEKGSPTILGVSKGEFLCYCDKXGSHPSLQ 120
DB 76 NLIAVPDKNYIRPEIFALASSLSASAEKGSPTILGVSKGEFLCYCDKXGSHPSLQ 135
QY 121 KKKKMLKLAOKESARRPIFYRAQVGSNMWLESAAHPGWFICTSCNCPNPEVGTDKFEN 180
DB 136 KKKKMLKLAOKESARRPIFYRAQVGSNMWLESAAHPGWFICTSCNCPNPEVGTDKFEN 195
QY 181 RKHIEFSFQVCKAEKMSPEVSD 203
DB 196 RKHIEFSFQVCKAEKMSPEVSD 218

RESULT 4
US-09-128-155-7
Sequence 7, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 167
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-7

Query Match
Best Local Similarity 66.3%; Score 702; DB 3; Length 167;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 64 AVDPKNYIRPEIFALASSLSASAEKGSPTILGVSKGEFLCYCDKXGSHPSLQKKE 123
DB 28 SLPTMNFVHTKIFALASSLSASAEKGSPTILGVSKGEFLCYCDKXGSHPSLQKKE 87
QY 124 KLMKLAOKESARRPIFYRAQVGSNMWLESAAHPGWFICTSCNCPNPEVGTDKFENRKH 183
DB 88 KLMKLAOKESARRPIFYRAQVGSNMWLESAAHPGWFICTSCNCPNPEVGTDKFENRKH 147
QY 184 IEFSPQVCKAEKMSPEVSD 203
DB 148 IEFSPQVCKAEKMSPEVSD 167

RESULT 5
US-09-128-155-2
Sequence 2, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-2

Query Match
Best Local Similarity 66.3%; Score 702; DB 3; Length 178;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 64 AVDPKNYIRPEIFALASSLSASAEKGSPTILGVSKGEFLCYCDKXGSHPSLQKKE 123
DB 39 SLPTMNFVHTKIFALASSLSASAEKGSPTILGVSKGEFLCYCDKXGSHPSLQKKE 98
QY 124 KLMKLAOKESARRPIFYRAQVGSNMWLESAAHPGWFICTSCNCPNPEVGTDKFENRKH 183
DB 99 KLMKLAOKESARRPIFYRAQVGSNMWLESAAHPGWFICTSCNCPNPEVGTDKFENRKH 158
QY 184 IEFSPQVCKAEKMSPEVSD 203
DB 159 IEFSPQVCKAEKMSPEVSD 178

RESULT 6
US-09-128-155-11
; Sequence 11, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-11

Query Match 65.6%; Score 695; DB 3; Length 136;
Best Local Similarity 96.3%; Pred. No. 1.4e-73;
Matches 130; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 69 NYIRPEIFALASSLSASAEKSPILLGVSGEFCLYCDKDGQSHPSLQKKKMKL 128
Db 2 NFVHTKFFALASSLSASAEKSPILLGVSGEFCLYCDKDGQSHPSLQKKKMKL 61
Qy 129 AAKESARPFIFYRAQVGNMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSF 188
Db 62 AAQESARPFIFYRAQVGNMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSF 121
Qy 189 QPVCKAEMSPSEVS 203
Db 122 QPVCKAEMSPSEVS 136

RESULT 7
US-09-128-155-5
; Sequence 5, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-5

Query Match 58.8%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-65;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 89 EKSPILLGVSGEFCLYCDKDGQSHPSLQKKKMKLAQKESARPFIFYRAQVGS 148
Db 1 EKSPILLGVSGEFCLYCDKDGQSHPSLQKKKMKLAQKESARPFIFYRAQVGS 60
Qy 149 NMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSFPVCKAEMSPSEVS 203
Db 61 NMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSFPVCKAEMSPSEVS 115

Db 61 NMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSFPVCKAEMSPSEVS 115
RESULT 8
US-09-128-155-9
; Sequence 9, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-9

Query Match 58.8%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-65;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 EKSPILLGVSGEFCLYCDKDGQSHPSLQKKKMKLAQKESARPFIFYRAQVGS 148
Db 1 EKSPILLGVSGEFCLYCDKDGQSHPSLQKKKMKLAQKESARPFIFYRAQVGS 60
Qy 149 NMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSFPVCKAEMSPSEVS 203
Db 61 NMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSFPVCKAEMSPSEVS 115

RESULT 9
US-09-128-155-13
; Sequence 13, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-13

Query Match 58.8%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-65;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 89 EKSPILLGVSGEFCLYCDKDGQSHPSLQKKKMKLAQKESARPFIFYRAQVGS 148
Db 1 EKSPILLGVSGEFCLYCDKDGQSHPSLQKKKMKLAQKESARPFIFYRAQVGS 60
Qy 149 NMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSFPVCKAEMSPSEVS 203
Db 61 NMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSFPVCKAEMSPSEVS 115

RESULT 10
US-09-128-155-18
Sequence 18, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: synthetically generated
LOCATION: (1)...(185)
OTHER INFORMATION: human sequence predicted using an alignment algorithm which
OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of
OTHER INFORMATION: interest in a stretch of genomic DNA
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(185)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-128-155-18
Query Match 44.7%; Score 473.5; DB 3; Length 185;
Best Local Similarity 91.8%; Pred. No. 2,1e-47;
Matches 90; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
QY 79 LASSLSASAEKSPILLGVSKGFCLYCDKDGSHPSIQLKKEKLMKLAQKESARRP 138
DB 71 LSSLQASASAEKSPILLGVSKGFCLYCDKDGSHPSIQLKKEKLMKLAQKESARRP 129
QY 139 FIFRYAQVGSWMNLESAHPGWFICTSCNCEPVGVTDK 176
DB 130 FIFRYAQVGSWMNLESAHPGWFICTSCNCEPVGIXN 167
RESULT 11
US-08-790-032-2
Sequence 2, Application US/08790032
Patent No. 5863769
GENERAL INFORMATION:
APPLICANT: Young, Peter
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
TITLE OF INVENTION: Beta (IL-1RA)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,032
FILING DATE: 28-JAN-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: ATG50051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5031
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-790-032-2
Query Match 21.7%; Score 229.5; DB 2; Length 169;
Best Local Similarity 35.0%; Pred. No. 7,5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;
QY 19 DDDDKLAANSALCRGPVKVNLNPKKFSIHDDQKVLVDSGNLJAVPDKNYIRPEIFPA 78
DB 7 DADGGRAVYQSMCK-----PIGTINDLNQVWTLQGNLVAVPRSDVTPVTAV 58
QY 79 LASSLSASAE-KGSFILLGVSKGFCLYCDKDGSHPSIQLKKEKLMKLAQKESARR 137
DB 59 ITCKYPEALEQGGDIYIGIQNPEMCLYCEKVGEG-PTLQKKEKINDLVGGQPEPV-K 115
QY 138 FIFRYAQVGSWMNLESAHPGWFICTSCNCEPVGVTDK 177
DB 116 PLFIFYRAKTRGTSTLESVAFPDWFIASS-KRQGPILLTSE 154
RESULT 12
US-09-069-619-2
Sequence 2, Application US/09069619
Patent No. 6054559
GENERAL INFORMATION:
APPLICANT: Young, Peter and Lisa Marshall
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
TITLE OF INVENTION: Beta (IL-1RA)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,619
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/007,464; and 08/790,032
FILING DATE: filed 14-JAN-1998; and 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William, T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50051-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-069-619-2

Query Match 21.7%; Score 229.5; DB 3; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;

Qy 19 DDDDKLAANAALCRGPKVKLNLPKFSIHDDHKVVLVDSGNLIAVDPDKYIRPEIFFA 78
Db 7 DADGGGRAVYQSMCK-----PITGTINDLNQVWTLQGNLVAVPRSDSVTPVTAV 58
Qy 79 LASSLSASAE-KSPILLGVSKGEFCLYCDKQSHPSIQLKKEKLMKLAQKESARR 137
Db 59 ITCKYPALEGRDPIYLGIQNPENCLYCEKVEQ--PTIQLKEQKIMDIYQPEPV-K 115
Qy 138 PFIFYRAQVGSMMLESAAHPGWFICTSCNCPNPEVGTDK 177
Db 116 PFLFYRAKTGRTSTLESVAFPDMFTASS-KRDQPIILTSE 154

RESULT 13
US-09-494-018-2

; Sequence 2, Application US/09494018
; Patent No. 6399573
; GENERAL INFORMATION:
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST BETA
; FILE REFERENCE: ATG-50051-D1
; CURRENT APPLICATION NUMBER: US/09/494,018
; EARLIER FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 09/069,619
; EARLIER FILING DATE: 1998-04-29
; EARLIER APPLICATION NUMBER: 09/007,464
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 08/790,032
; EARLIER FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 169
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-494-018-2

Query Match 21.7%; Score 229.5; DB 4; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;

Qy 19 DDDDKLAANAALCRGPKVKLNLPKFSIHDDHKVVLVDSGNLIAVDPDKYIRPEIFFA 78
Db 7 DADGGGRAVYQSMCK-----PITGTINDLNQVWTLQGNLVAVPRSDSVTPVTAV 58
Qy 79 LASSLSASAE-KSPILLGVSKGEFCLYCDKQSHPSIQLKKEKLMKLAQKESARR 137
Db 59 ITCKYPALEGRDPIYLGIQNPENCLYCEKVEQ--PTIQLKEQKIMDIYQPEPV-K 115
Qy 138 PFIFYRAQVGSMMLESAAHPGWFICTSCNCPNPEVGTDK 177
Db 116 PFLFYRAKTGRTSTLESVAFPDMFTASS-KRDQPIILTSE 154

RESULT 14
US-09-398-412B-15
; Sequence 15, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:

; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reager
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-15

Query Match 21.7%; Score 229.5; DB 4; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;

Qy 19 DDDDKLAANAALCRGPKVKLNLPKFSIHDDHKVVLVDSGNLIAVDPDKYIRPEIFFA 78
Db 7 DADGGGRAVYQSMCK-----PITGTINDLNQVWTLQGNLVAVPRSDSVTPVTAV 58
Qy 79 LASSLSASAE-KSPILLGVSKGEFCLYCDKQSHPSIQLKKEKLMKLAQKESARR 137
Db 59 ITCKYPALEGRDPIYLGIQNPENCLYCEKVEQ--PTIQLKEQKIMDIYQPEPV-K 115
Qy 138 PFIFYRAQVGSMMLESAAHPGWFICTSCNCPNPEVGTDK 177
Db 116 PFLFYRAKTGRTSTLESVAFPDMFTASS-KRDQPIILTSE 154

RESULT 15
US-09-398-412B-13

; Sequence 13, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reager
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-398-412B-13

Query Match 18.1%; Score 191.5; DB 4; Length 156;
Best Local Similarity 35.1%; Pred. No. 1.9e-14;
Matches 53; Conservative 24; Mismatches 51; Indels 23; Gaps 6;

Qy 28 NSALCRGPKVKLNLPKFSIHDDHKVVLVDSGNLIAVDPDKYIRPEIFALASSLS 85
Db 5 SGNLC-----FRMKDSALTKVLIHNNQLLAGLHAKEVIGELISVPRNALD 52
Qy 86 ASAEKSPILLGVSKGEFCLYCDKQSHPSIQLKKEKLMKLAQKESARRPFIYRA 144
Db 53 ASL---SPVILGVQSGQCLSCGTEKG---PIKLLEPVNIMELYLAKEG--KSFYFRR 104
Qy 145 QVGSMMLESAAHPGWFICTSCNCPNPEVGT 175
Db 105 DMGLTSSFESAAYPGWFLCTSPADQPVRLT 135

Search completed: September 9, 2004, 13:29:59
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:23:09 ; Search time 48 Seconds

(without alignments)
1356.250 Million cell updates/sec

Title: US-09-869-566-5

Perfect score: 1059
Sequence: 1 MSALLILALVNAAYDYKD.....IEFSFQPCVKAEMSPSEUSD 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	906	85.6	192	10	US-09-876-790-3
2	906	85.6	192	14	US-10-139-833-13
3	902	85.2	197	10	US-09-876-790-9
4	895	84.5	198	9	US-09-788-963-6
5	895	84.5	218	9	US-09-788-963-2
6	895	84.5	218	10	US-09-876-790-8
7	895	84.5	218	12	US-10-695-195-4
8	895	84.5	218	14	US-10-139-833-12
9	895	84.5	218	14	US-10-302-554-2
10	895	84.5	218	16	US-10-694-978-4
11	895	84.5	218	16	US-10-679-201-6
12	891	84.1	218	14	US-10-302-554-14
13	885	83.6	193	12	US-10-063-745-142
14	885	83.6	193	12	US-10-063-512-142
15	885	83.6	193	12	US-10-063-513-142

16	885	83.6	193	12	US-10-063-515-142	Sequence 142, App
17	885	83.6	193	12	US-10-063-549-142	Sequence 142, App
18	885	83.6	193	12	US-10-063-569-142	Sequence 142, App
19	885	83.6	193	12	US-10-063-551-142	Sequence 142, App
20	885	83.6	193	12	US-10-063-555-142	Sequence 142, App
21	885	83.6	193	12	US-10-063-563-142	Sequence 142, App
22	885	83.6	193	12	US-10-063-594-142	Sequence 142, App
23	885	83.6	193	12	US-10-063-553-142	Sequence 142, App
24	885	83.6	193	12	US-10-063-554-142	Sequence 142, App
25	885	83.6	193	13	US-10-006-867-142	Sequence 142, App
26	885	83.6	193	13	US-10-063-547-142	Sequence 142, App
27	885	83.6	193	14	US-10-063-616-142	Sequence 142, App
28	885	83.6	193	14	US-10-063-502-142	Sequence 142, App
29	885	83.6	193	14	US-10-063-518-142	Sequence 142, App
30	885	83.6	193	14	US-10-063-598-142	Sequence 142, App
31	885	83.6	193	14	US-10-227-693-142	Sequence 142, App
32	885	83.6	193	14	US-10-063-567-142	Sequence 142, App
33	885	83.6	193	14	US-10-063-538-142	Sequence 142, App
34	885	83.6	193	14	US-10-063-599-142	Sequence 142, App
35	885	83.6	193	14	US-10-063-595-142	Sequence 142, App
36	885	83.6	193	14	US-10-063-580-142	Sequence 142, App
37	885	83.6	193	14	US-10-063-557-142	Sequence 142, App
38	885	83.6	193	14	US-10-063-585-142	Sequence 142, App
39	885	83.6	193	14	US-10-063-588-142	Sequence 142, App
40	885	83.6	193	14	US-10-063-735-142	Sequence 142, App
41	885	83.6	193	14	US-10-063-526-142	Sequence 142, App
42	885	83.6	193	14	US-10-063-586-142	Sequence 142, App
43	885	83.6	193	14	US-10-063-546-142	Sequence 142, App
44	885	83.6	193	14	US-10-063-564-142	Sequence 142, App
45	885	83.6	193	14	US-10-063-662-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-09-876-790-3
Sequence 3, Application US/09876790
Publication No. US2003091532A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECE DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent version 3.1
SEQ ID NO 3
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-3

Query Match 85.6%; Score 906; DB 10; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.7e-91;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	33	RGPRVKLNLPKFFIHDDHVLVDSCNLIAPVDKVIIRPEIFPALASSISAAKGS	92
Db	22	RGPRVKLNLPKFFIHDDHVLVDSCNLIAPVDKVIIRPEIFPALASSISAAKGS	81
Qy	93	PILGVSGKEFCVCDKDKGSHPSLQKKKEKMLAAQKESARPFIFRAQGVNML	152
Db	82	PILGVSGKEFCVCDKDKGSHPSLQKKKEKMLAAQKESARPFIFRAQGVNML	141

QY 153 ESAHHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 203
DB 142 ESAHHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 192

RESULT 2

US-10-139-833-13
Sequence 13, Application US/10139833
Publication No. US20030004106A1
GENERAL INFORMATION:
APPLICANT: Satrio, Christiaan M.
APPLICANT: Gales, Jennifer
APPLICANT: Mu, Sharon X.
APPLICANT: Xia, Min
APPLICANT: Baes, Michael B.
APPLICANT: Craveiro, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
FILE REFERENCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139, 833
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/170,191
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/188,053
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/194,521
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 60/195,910
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724,583
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 13
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-10-139-833-13

Query Match 85.6%; Score 906; DB 14; Length 192;
Best Local Similarity 100.0%; Pred. No. 4,7e-91;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 RGRKVNLPKPKFSIHDDHKLVLVDGNTLAVDPKNYIRPEIFPALASSLSASAEGKS 92
DB 22 RGRKVNLPKPKFSIHDDHKLVLVDGNTLAVDPKNYIRPEIFPALASSLSASAEGKS 81
QY 93 PILGVSKGFCLYCDKQKQSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNNML 152
DB 82 PILGVSKGFCLYCDKQKQSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNNML 141
QY 153 ESAHHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 203
DB 142 ESAHHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 192

RESULT 3

US-09-876-790-9
Sequence 9, Application US/09876790
Publication No. US20030091532A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECE2 DNAS AND POLYPEPT
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/09/876,790
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549

PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In version 3.1
SEQ ID NO 9
LENGTH: 197
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-9

Query Match 85.2%; Score 902; DB 10; Length 197;
Best Local Similarity 91.5%; Pred. No. 1.4e-90;
Matches 17; Conservative 4; Mismatches 6; Indels 6; Gaps 1;

QY 16 DYKDDDKLAAANSALCRGPKVKNLPPKFSIHDDHKLVLVDGNTLAVDPKNYIRPEI 75
DB 16 DWEKDEPQ-----CLEGPKVKNLPPKFSIHDDHKLVLVDGNTLAVDPKNYIRPEI 69
QY 76 FFALASSLSASAEGKSPILGVSKGFCLYCDKQKQSHPSLQKKKMLKLAQKESA 135
DB 70 FFALASSLSASAEGKSPILGVSKGFCLYCDKQKQSHPSLQKKKMLKLAQKESA 129
QY 136 RRPFIYRAQVGSNNMLESAHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQVCKAE 195
DB 130 RRPFIYRAQVGSNNMLESAHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQVCKAE 189
QY 196 MSPSEVSD 203
DB 190 MSPSEVSD 197

RESULT 4

US-09-788-963-6
Sequence 6, Application US/09788963
Patent No. US20020052473A1
GENERAL INFORMATION:
APPLICANT: YOUNG, PETER R.
APPLICANT: McDONNELL, PETER C.
APPLICANT: KUMAR, SANJAY
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
FILE REFERENCE: GP-70607-1C1
CURRENT APPLICATION NUMBER: US/09/788,963
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/293,625
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 09/452,140
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 198
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-788-963-6

Query Match 84.5%; Score 895; DB 9; Length 198;
Best Local Similarity 100.0%; Pred. No. 8e-90;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKYKNLPKPKFSIHDDHKLVLVDGNTLAVDPKNYIRPEIFPALASSLSASAEGKSP 94
DB 30 PKYKNLPKPKFSIHDDHKLVLVDGNTLAVDPKNYIRPEIFPALASSLSASAEGKSP 89
QY 95 ILGVSKGFCLYCDKQKQSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNNML 154
DB 90 ILGVSKGFCLYCDKQKQSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNNML 149
QY 155 AAHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 203
DB 150 AAHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQVCKAEMSPSEVSD 198

RESULT 5

US-09-788-963-2

Sequence 2, Application us/09788963
Patent No. US20020052473A1
GENERAL INFORMATION:
APPLICANT: YOUNG, PETER R.
APPLICANT: MCDONNELL, PETER C.
APPLICANT: KUMAR, SANJAY
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
FILE REFERENCE: GP-70607-1C1
CURRENT APPLICATION NUMBER: US/09/788,963
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/293,625
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 09/452,140
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-788-963-2

Query Match 84.5%; Score 895; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 PKVKNLNPKKFSIHQDHKVLVDSGNLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 94
Db 50 PKVKNLNPKKFSIHQDHKVLVDSGNLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 109
Qy 95 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 154
Db 110 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 169
Qy 155 AAHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFPVCKAEMSPSEVSD 203
Db 170 AAHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFPVCKAEMSPSEVSD 218

RESULT 6
US-09-876-790-8
Sequence 8, Application US/09876790
Publication No. US20030091532A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECE DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/09/876,790
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-8

Query Match 84.5%; Score 895; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 PKVKNLNPKKFSIHQDHKVLVDSGNLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 94
Db 50 PKVKNLNPKKFSIHQDHKVLVDSGNLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 109

Qy 95 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 154
Db 110 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 169
Qy 155 AAHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFPVCKAEMSPSEVSD 203
Db 170 AAHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFPVCKAEMSPSEVSD 218

RESULT 7
US-10-695-195-4
Sequence 4, Application US/10695195
Publication No. US20040068099A1
GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-695-195-4

Query Match 84.5%; Score 895; DB 12; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 PKVKNLNPKKFSIHQDHKVLVDSGNLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 94
Db 50 PKVKNLNPKKFSIHQDHKVLVDSGNLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 109
Qy 95 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 154
Db 110 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 169
Qy 155 AAHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFPVCKAEMSPSEVSD 203
Db 170 AAHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFPVCKAEMSPSEVSD 218

RESULT 8
US-10-139-833-12
Sequence 12, Application US/10139833
Publication No. US20030004106A1

```

GENERAL INFORMATION:
APPLICANT: Saris, Christiaan M.
APPLICANT: Giles, Jennifer
APPLICANT: Wu, Sharon X.
APPLICANT: Xia, Min
APPLICANT: Bass, Michael B.
APPLICANT: Cavetiro, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
FILE REFERENCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139,833
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/170,191
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/188,053
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/194,521
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 60/195,910
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724,583
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-139-833-12

```

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Query Match      84.5%; Score 895; DB 14; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 35 PKYKLNPPKFSIHDDHKLVLVDGSLVAVDPKNYIREIFPALLASSLSASAEGSP1 94

DB 50 PKYKLNPPKFSIHDDHKLVLVDGSLVAVDPKNYIREIFPALLASSLSASAEGSP1 109

QY 95 LIGVSKGEFLCYCDKXGSHPSLQJKEKLMKLAQAQESARRPFIYRAQVGSNMLES 154

DB 110 LIGVSKGEFLCYCDKXGSHPSLQJKEKLMKLAQAQESARRPFIYRAQVGSNMLES 169

QY 155 AAHPGWFICTSCNCPNPEVGTDKFENRKHIIEFSFQVCAEMSPSEVSD 203

DB 170 AAHPGWFICTSCNCPNPEVGTDKFENRKHIIEFSFQVCAEMSPSEVSD 218

```

RESULT 9
US-10-302-554-2
Sequence 2, Application US/10302554
Publication No. US20030148467A1
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
FILE REFERENCE: 98-59
CURRENT APPLICATION NUMBER: US/10/302,554
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/428,118
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 60/105,824
PRIOR FILING DATE: 1998-10-27
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-302-554-2

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Query Match      84.5%; Score 895; DB 14; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90;

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Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 35 PKYKLNPPKFSIHDDHKLVLVDGSLVAVDPKNYIREIFPALLASSLSASAEGSP1 94

DB 50 PKYKLNPPKFSIHDDHKLVLVDGSLVAVDPKNYIREIFPALLASSLSASAEGSP1 109

QY 95 LIGVSKGEFLCYCDKXGSHPSLQJKEKLMKLAQAQESARRPFIYRAQVGSNMLES 154

DB 110 LIGVSKGEFLCYCDKXGSHPSLQJKEKLMKLAQAQESARRPFIYRAQVGSNMLES 169

QY 155 AAHPGWFICTSCNCPNPEVGTDKFENRKHIIEFSFQVCAEMSPSEVSD 203

DB 170 AAHPGWFICTSCNCPNPEVGTDKFENRKHIIEFSFQVCAEMSPSEVSD 218

```

RESULT 10
US-10-694-978-4
Sequence 4, Application US/10694978
Publication No. US20040087766A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-694-978-4

```

```

Query Match      84.5%; Score 895; DB 16; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 35 PKYKLNPPKFSIHDDHKLVLVDGSLVAVDPKNYIREIFPALLASSLSASAEGSP1 94

DB 50 PKYKLNPPKFSIHDDHKLVLVDGSLVAVDPKNYIREIFPALLASSLSASAEGSP1 109

QY 95 LIGVSKGEFLCYCDKXGSHPSLQJKEKLMKLAQAQESARRPFIYRAQVGSNMLES 154

DB 110 LIGVSKGEFLCYCDKXGSHPSLQJKEKLMKLAQAQESARRPFIYRAQVGSNMLES 169

QY 155 AAHPGWFICTSCNCPNPEVGTDKFENRKHIIEFSFQVCAEMSPSEVSD 203

DB 170 AAHPGWFICTSCNCPNPEVGTDKFENRKHIIEFSFQVCAEMSPSEVSD 218

; CURRENT APPLICATION NUMBER: US/10/063,512
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 142
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-063-512-142

Query Match 83.6%; Score 885; DB 12; Length 193;
 Best Local Similarity 99.4%; Pred. No. 9,7e-89;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 KVNKLNPKKFSIHQDQHKVLVLDGNIIVADPKYIRPEIFPALASSLSASAEKGSPTL 95
 :
 Db 26 RVKKNLNPKKFSIHQDQHKVLVLDGNIIVADPKYIRPEIFPALASSLSASAEKGSPTL 85
 QY 96 LGVSKGEFLCYCDKDKQSHPSLQKKKKLMLAOKESARPPFIFFRAQVGSNMLESA 155
 :
 Db 86 LGVSKGEFLCYCDKDKQSHPSLQKKKKLMLAOKESARPPFIFFRAQVGSNMLESA 145
 QY 156 AHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
 :
 Db 146 AHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 193

RESULT 15

US-10-063-513-142
 ; Sequence 142, Application US/10063513
 ; Publication No. US20030018172A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P9230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,513
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 142
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-063-513-142

Query Match 83.6%; Score 885; DB 12; Length 193;
 Best Local Similarity 99.4%; Pred. No. 9,7e-89;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 KVNKLNPKKFSIHQDQHKVLVLDGNIIVADPKYIRPEIFPALASSLSASAEKGSPTL 95
 :
 Db 26 RVKKNLNPKKFSIHQDQHKVLVLDGNIIVADPKYIRPEIFPALASSLSASAEKGSPTL 85
 QY 96 LGVSKGEFLCYCDKDKQSHPSLQKKKKLMLAOKESARPPFIFFRAQVGSNMLESA 155
 :
 Db 86 LGVSKGEFLCYCDKDKQSHPSLQKKKKLMLAOKESARPPFIFFRAQVGSNMLESA 145
 QY 156 AHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
 :
 Db 146 AHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 193

Search completed: September 9, 2004, 13:29:22
 Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:11:59 / Search time 123 Seconds
(without alignments)
466.318 Million cell updates/sec

Title: US-09-869-566-5
Perfect score: 1059
Sequence: 1 MSALLILATVGAADVADYKDD.....IEFSFPVKAKEMSPSEVSD 203

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

1:	geneeqp1980s:*
2:	geneeqp1990s:*
3:	geneeqp2000s:*
4:	geneeqp2001s:*
5:	geneeqp2002s:*
6:	geneeqp2003as:*
7:	geneeqp2003bs:*
8:	geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1059	100.0	203	3	AAV96933 Human IL-
2	906	85.6	192	3	AAV95297 Human int
3	902	85.2	197	3	AAV95300 Human int
4	895	84.5	198	4	AAV95300 Human int
5	895	84.5	207	3	AAV96938 Human IL-
6	895	84.5	218	3	AAV70927 Human int
7	895	84.5	218	3	AAV91885 Primate i
8	895	84.5	218	3	AAV95299 Human int
9	895	84.5	218	3	AAV96940 Human IL-
10	895	84.5	218	3	AAV96940 Human IL-
11	895	84.5	218	4	AAV96940 Human int
12	895	84.5	218	4	AAV96940 Human int
13	895	84.5	218	4	AAV96940 Human int
14	895	84.5	218	4	AAV96940 Human int
15	895	84.5	218	4	AAV96940 Human int
16	895	84.5	218	4	AAV96940 Human int
17	895	84.5	218	4	AAV96940 Human int
18	895	84.5	218	4	AAV96940 Human int
19	895	84.5	218	4	AAV96940 Human int
20	895	84.5	218	4	AAV96940 Human int
21	895	84.5	218	4	AAV96940 Human int
22	895	84.5	218	4	AAV96940 Human int
23	895	84.5	218	4	AAV96940 Human int
24	895	84.5	218	4	AAV96940 Human int
25	895	84.5	218	4	AAV96940 Human int

26	885	83.6	193	6	ABU81216 Human sec
27	885	83.6	193	6	ABO53330 Novel hum
28	885	83.6	193	6	ABU98333 Novel hum
29	885	83.6	193	6	ABU89338 Novel hum
30	885	83.6	193	6	ABU82545 Novel hum
31	885	83.6	193	6	ABU96509 Human PRO
32	885	83.6	193	6	ABU72179 Human PRO
33	885	83.6	193	6	ADBI17199 Human tra
34	885	83.6	193	6	ABO44309 Human sec
35	885	83.6	193	6	ADA20004 Novel hum
36	885	83.6	193	6	ADBI17387 Human tra
37	885	83.6	193	6	ADA20176 Novel hum
38	885	83.6	193	6	ABO34237 Human sec
39	885	83.6	193	6	ADA00473 Human sec
40	885	83.6	193	6	ADBI17199 Human tra
41	885	83.6	193	7	ADBI17199 Human tra
42	885	83.6	193	7	ADBI17199 Human tra
43	885	83.6	193	7	ADBI17199 Human tra
44	885	83.6	193	7	ADBI17199 Human tra
45	885	83.6	193	7	ADBI17199 Human tra

ALIGNMENTS

RESULT 1
ID AAV96933 standard; protein: 203 AA.
XX AAV96933;
DT 31-OCT-2000 (first entry)
XX Human IL-1RA fused to heterologous signal sequence.
DE Human IL-1RA fused to heterologous signal sequence.
XX hIL-1RA; human interleukin-1 receptor antagonist-1; IL-1p; osteopontin;
KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW anti-arthritic; antimicrobial; respiratory; anti-ischemic; vaccine;
KW dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..15
FT Peptide /label= Signal_peptide
FT Peptide 16..23
FT Peptide /label= Flag_tag
FT Peptide 24..36
FT Peptide /label= linker
FT Protein 37..203
FT /label= hIL-1RA1
XX WO200039297-A2.
XX 06-JUL-2000.
XX 22-DEC-1999; 99KO-US030720.
XX 23-DEC-1998; 98US-0113430P.
XX 22-JAN-1999; 99US-0116843P.
XX 13-APR-1999; 99US-0129122P.
XX (GETH) GENENTECH INC.
XX Goddard A, Pan J; Audrey
XX WPI; 2000-452395/39.
XX N-PSDB; AAA51592.
XX Nucleic acid encoding interleukin-1-like polypeptides, useful for
FT preventing and treating e.g. inflammation, asthma and psoriasis.
XX Claim 22; Fig 2; 143pp; English.
PS

XX An isolated nucleic acid molecule encoding an interleukin-1-like
 CC polypeptide (IL-11p) that retains one or more activities of the peptide
 CC from which it is derived, such as the IL-18R binding activity of a human
 CC interleukin-1 receptor antagonist-1 (IL-1Ra1) polypeptide, is new. The
 CC nucleic acids may be used in molecular engineering applications, e.g.
 CC hybridization assays and chromosome and gene mapping studies, for
 CC recombinantly producing the IL-11p polypeptide or for producing gene
 CC knock out animals to study the role of the protein in metabolism and
 CC disease processes (conversely, gene therapy protocols may be used to
 CC supplement a patient's production of the polypeptide or to rectify
 CC mutations that lead to the production of an active peptide). The
 CC peptides produced may be used to screen for and produce modulators (e.g.
 CC antibodies) of IL-11p protein expression and activity which may be use to
 CC treat disorders associated with inappropriate IL-11p expression and
 CC activity, such as inflammatory disorders, asthma, arthritis, and
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease
 CC XX

SQ Sequence 203 AA:

Query Match 100.0%; Score 1059; DB 3; Length 203;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSALLILALVGAADVADYKDDDDKLAANASALCGPKVKNLNPKKFSIHDDHKVLYVDSG 60
 Db 1 MSALLILALVGAADVADYKDDDDKLAANASALCGPKVKNLNPKKFSIHDDHKVLYVDSG 60
 QY 61 NLIAVDDKNVIRPEIFFALASSLSASAEKGSPIILGVSKGEFCLYCDKDKGSHPSLQL 120
 Db 61 NLIAVDDKNVIRPEIFFALASSLSASAEKGSPIILGVSKGEFCLYCDKDKGSHPSLQL 120
 QY 121 KKKKMLKLAQKESARRPFIFRYAQVGSWMLESAAHPGFICTSCNCEPVGTTDKFEN 180
 Db 121 KKKKMLKLAQKESARRPFIFRYAQVGSWMLESAAHPGFICTSCNCEPVGTTDKFEN 180
 QY 181 RKHIEFSFQVCAKEMSPSEVSD 203
 Db 181 RKHIEFSFQVCAKEMSPSEVSD 203

RESULT 2

AA95297
 ID AAY95297 standard; protein; 192 AA.

AC AAY95297;

DT 12-SEP-2000 (first entry)

DE Human interleukin-1 zeta.

XX Interleukin-1 zeta; IL-1 zeta; human; therapy; inflammation; fever.

OS Homo sapiens.

PN WO200036108-A2.

PD 22-JUN-2000.

PF 14-DEC-1999; 99WO-US029549.

PR 14-DEC-1998; 98US-0112163P.

PR 10-NOV-1999; 99US-0164675P.

PA (IMMV) IMMUNEX CORP.

PI Sims JB, Smith DE, Born TL;

XX WPI; 2000-442387/38.

DR N-PSDB; AAA27918.

XX

PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
 PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
 PT identifying genes associated with diseases such as glaucoma, and insulin-
 PT dependent diabetes mellitus.

PS Claim 10, Page 8; 87pp; English.

XX The present sequence is that of human interleukin-1 zeta (IL-1 zeta), a
 CC member of the IL-1 family. The sequence was determined by translation of
 CC the nucleotide sequence of isolated IL-1 zeta cDNA (see AAA27918). IL-1
 CC zeta mRNA is generated from exons 3-6 of the IL-1 zeta locus. The mRNA is
 CC expressed most strongly in the testis, prostate, colon, brain, placenta,
 CC lung, foetal liver and lymph node stroma, lung, testis and placenta. The
 CC invention is directed to novel, purified and isolated IL-1 zeta, IL-1
 CC zeta splice variants and Xrec2 polypeptides (see AAY95297-301), the
 CC nucleic acids (see AAA27918-22) encoding such polypeptides, processes for
 CC production of recombinant forms of such polypeptides, and their uses. The
 CC polypeptides can be used to study cellular processes such as immune
 CC regulation, cell proliferation, cell death, cell migration, cell-to-cell
 CC interaction and inflammatory responses, to identify proteins associated
 CC with IL-1 zeta, to screen for potential inhibitors, and to prepare
 CC antibodies. In particular, they can be used to activate and/or inhibit
 CC the activation of vascular endothelial cells and lymphocytes, induce
 CC and/or inhibit the induction of local tissue destruction and fever,
 CC inhibit and/or stimulate macrophages and vascular endothelial cells to
 CC produce IL-6, induce and/or inhibit the induction of prostaglandins,
 CC nitric oxide synthetase, and metalloproteinases, and upregulate and/or
 CC inhibit the upregulation of molecules on the surface of vascular
 CC endothelial cells
 CC XX

SQ Sequence 192 AA:

Query Match 85.6%; Score 906; DB 3; Length 192;
 Best Local Similarity 100.0%; Pred. No. 8.4e-96;
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 RGPKNVNLNPKKFSIHDDHKVLYVDSGNLIAVPDKNVIRPEIFFALASSLSASAEKGS 92
 Db 22 RGPKNVNLNPKKFSIHDDHKVLYVDSGNLIAVPDKNVIRPEIFFALASSLSASAEKGS 81
 QY 93 PILGVSKGEFCLYCDKDKGSHPSLQLKKKMLKLAQKESARRPFIFRYAQVGSWMNL 152
 Db 82 PILGVSKGEFCLYCDKDKGSHPSLQLKKKMLKLAQKESARRPFIFRYAQVGSWMNL 141
 QY 153 ESAAHPGFICTSCNCEPVGTTDKFENRKHIEFSFQVCAKEMSPSEVSD 203
 Db 142 ESAAHPGFICTSCNCEPVGTTDKFENRKHIEFSFQVCAKEMSPSEVSD 192

RESULT 3

AA95300
 ID AAY95300 standard; protein; 197 AA.

AC AAY95300;

DT 12-SEP-2000 (first entry)

DE Human interleukin-1 zeta splice variant TDZ.2.

XX Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.2;

KW testis-derived zeta variant; therapy; inflammation; fever.

OS Homo sapiens.

PN WO200036108-A2.

PD 22-JUN-2000.

PF 14-DEC-1999; 99WO-US029549.

PR 14-DEC-1998; 98US-0112163P.

PR 10-NOV-1999; 99US-0164675P.

XX

Query Match	85.2%	Score 902	DB 3	Length 197
Best Local Similarity	91.5%	Pred. No. 2.5e-95		
Matches 172	Conservative 4	Mismatches 6	Indels 6	Gaps 1
QY	16 DYKDDDDKLAANSLACRGPKYKNNLPKKFSIHDDHRYVLVDSGNLAVDPKYYIREI	75		
DB	16 DWEKDEPD-----CCLBGPKNKNNLPKKFSIHDDHRYVLVDSGNLAVDPKYYIREI	69		
QY	76 FFALASSSSASAEKSGPILLVGSGKGFCLYCDKXGQSHPSLQJKEKELMKLAQKESA	135		
DB	70 FFALASSSSASAEKSGPILLVGSGKGFCLYCDKXGQSHPSLQJKEKELMKLAQKESA	129		
QY	136 RRPFIIFYRAQVGSNMMLSEAAHPGMFICTSCNCEPVGVTDKFENRKHIIEFSFOVCKAE	195		
DB	130 RRPFIIFYRAQVGSNMMLSEAAHPGMFICTSCNCEPVGVTDKFENRKHIIEFSFOVCKAE	189		
QY	196 MSPSEVSD 203			
DB	190 MSPSEVSD 197			
RESULT 4				
AAAB85138				
ID	AAAB85138 standard; protein, 198 AA.			
AC	AAAB85138;			
XX				
XX	22-AUG-2001 (first entry)			
DE	Interleukin-1 homologue (IL-1H4) mature polypeptide.			
XX				
XX	Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;			
KM	immunopressive; antipsoaric; antiarthritic; cytostatic; antiHV;			
KM	cerebroprotective; antisthmatic; vasotropic; vulnary; osteopathic;			
KM	immunostimulant; antiatherosclerotic; nootropic; neuroprotective;			
KM	gene therapy; vaccine.			

XX	Homo sapiens.
OS	WO200140247-A1.
XX	
PN	07-JUN-2001.
PD	
XX	
Pf	30-NOV-2000; 2000MO-US032521.
XX	
PR	01-DEC-1999; 99US-00452140.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	
Kumar S, Mcdonnell PC, Young PR;	
XX	
PI	WPI, 2001-389949/41.
DR	
PT	Novel Interleukin-1 homolog, IL-1H4, for treating chronic and acute
XX	
PT	inflammation, septicemia, autoimmune diseases, transplant rejection,
XX	
PT	graft versus host disease, stroke, ischemia, allergy and asthma.
PS	
XX	
PS	Claim 1; Page 29; 30pp; English.
CC	
CC	The invention provides an isolated interleukin-1 homologue, IL-1H4
CC	polypeptide. The IL-1H4 polypeptide can be expressed by standard
CC	recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
CC	modulators are useful for treating chronic and acute inflammation,
CC	septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
CC	psoriasis and arthritis), transplant rejection, graft versus host
CC	disease, infection, stroke, ischemia, acute respiratory disease syndrome,
CC	allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
CC	osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
CC	heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
CC	polynucleotides are useful as diagnostic reagents and for chromosome
CC	identification. The present sequence represents the IL-1H4 mature
CC	polypeptide
SQ	
	Sequence 198 AA:
Query Match	84.5%; Score 895; DB 4; Length 198;
Best Local Similarity	100.0%; Pred. No. 1,6e-94;
Matches 169; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	35 PKVKNLNLKKESIHDDHKVLVLDSGNLIAVPDKNYIRPEIFPALASSLSASAEKSGSPI 94
Db	30 PKVKLNLPKKSISHDQHKVLVLDSGNLIAVPDKNYIRPEIFPALASSLSASAEKSGSPI 89
Oy	95 LLGYSKGFCILCYCDKDKQSHPISQLKKKKLMKLAOKESARRPFIPRAOVGSMMNLES 154
Db	90 LLGYSKGFCILCYCDKDKQSHPISQLKKKKLMKLAOKESARRPFIPRAOVGSMMNLES 149
Oy	155 AAPHGMFICTSCNCNEPVGVTDKEFNRRKHIEFFSOPVCKAEMSPSEVSVD 203
Db	150 AAPHGMFICTSCNCNEPVGVTDKEFNRRKHIEFFSOPVCKAEMSPSEVSVD 198
RESULT 5	
AAY96938	
ID	AAY96938 standard; protein; 207 AA.
XX	
AA96938;	
XX	
DT	31-OCT-2000 (first entry)
XX	
DE	Human IL-1 receptor antagonist 1 long.
XX	
Kw	hIL-1R α L; human interleukin-1 receptor antagonist-1 long; IL-1lp;
Kw	osteopethtic; interleukin-1-like polypeptide; anti-inflammatory;
Kw	anti-acathetic; anti-arthritis; antimicrobial; respiratory; vaccine;
Kw	anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
Kw	gene therapy.
XX	
OS	Homo sapiens.


```

XX 27-OCT-1998; 98US-00179614.
PR (ZYMO ) ZYMOGENETICS INC.
XX
XX West RR, Sheppard PO, Gao Z;
XX WPI; 2000-350740/30.
XX N-PSDB; AAD00210.
XX
XX Immunomodulatory interleukin-1 homolog zila4 proteins, useful for
XX treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
XX disease, leukemia.
XX
XX Claim 4; Fig 2; 88pp; English.
XX
XX The present sequence is the human interleukin (IL)-1 homolog zila4
XX protein. This protein contains a core structure of 12 beta-strands wound
XX into a beta-barrel, with the beta-strands separated from each other by
XX loops. The loops between these beta-strands are highly variable among the
XX family members and are believed to be involved in receptor binding. The
XX zila4 proteins modulate inflammation and other immunological processes
XX and are therefore useful for treatment of arthritis, psoriasis, septic
XX shock, graft-versus-host disease and leukemia. Other diseases that may
XX be modulated by zila4 proteins include cancer, anaemia, inflammatory
XX bowel disease, acute and chronic neuropathologies, shock, respiratory
XX disease syndrome, restenosis and acquired immune deficiency syndrome
XX
XX Sequence 218 AA;
SQ
Query Match 84.5%; Score 895; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 PKYKNLNPKKFSIHDDHKVLYLDSGNLAVPDKNYIRPEIFALASSLSASAEKGSPI 94
DB 50 PKYKNLNPKKFSIHDDHKVLYLDSGNLAVPDKNYIRPEIFALASSLSASAEKGSPI 109
QY 95 LLAGVSKGEFCLYCDKXGSHPSLQLKKEKMLAAQKESARRPFIYRAQVGSMMNLES 154
DB 110 LLAGVSKGEFCLYCDKXGSHPSLQLKKEKMLAAQKESARRPFIYRAQVGSMMNLES 169
QY 155 AAHPGFICTSCNCPNPGVGTDFENRKHIEFSFQPCAKEMSPSEVSD 203
DB 170 AAHPGFICTSCNCPNPGVGTDFENRKHIEFSFQPCAKEMSPSEVSD 218
RESULT 7
ID AAY91885 standard; protein; 218 AA.
XX
XX AAY91885;
XX
XX 19-JUL-2000 (first entry)
XX
XX Primate interleukin-1 like molecule (IL-1-zeta) alternative sequence.
XX
XX Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;
XX hypoglycemia; plasma iron; plasma zinc; acute liver response;
XX plasma copper.
XX
XX Mammalia.
XX
XX Key Location/Qualifiers
XX Domain 58..64
XX Domain /label= beta_strand_1
XX Domain 69..74
XX Domain /label= beta_strand_2
XX Domain 76..80
XX Domain /label= beta_strand_3
XX Domain 91..96
XX Domain /label= beta_strand_4
XX Binding-site 100..106

```

```

FT /note= "forms a loop which is part of a primary binding
FT segment to the IL-1 receptor type"
FT Domain 107..113
FT /label= beta_strand_5
FT Domain 118..126
FT /label= beta_strand_6
FT Domain 131..136
FT /label= beta_strand_7
FT Domain 154..161
FT /label= beta_strand_8
FT Domain 163..169
FT /label= beta_strand_9
FT Domain 176..180
FT /label= beta_strand_10
FT Domain 185..204
FT /label= beta_strand_11
FT Domain 201..204
FT /label= beta_strand_12
XX
XX WO200017363-A2.
XX
XX 30-MAR-2000.
XX
XX 17-SEP-1999; 99WO-US020868.
XX
XX 18-SEP-1998; 98US-00156966.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Timans JC;
XX
XX WPI; 2000-283588/24.
XX N-PSDB; AAA08513.
XX
XX New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful
XX for diagnostic and therapeutic purposes, comprises a 128 amino acid
XX sequence.
XX
XX Claim 1; Page 103-104; 110pp; English.
XX
XX The present sequence is an alternative primate interleukin-1 like
XX molecule, designated IL-1-zeta. The 12 beta strands, indicated in the
XX features table, fold into a beta-trefoil fold. The specification claims
XX an isolated or recombinant polypeptide that: (a) specifically binds
XX polyclonal antibodies generated against at least a 12 consecutive amino
XX acid segment of IL-1-zeta (see AAY91884) or its allelic variant (see
XX AAY91885); and (b) comprises at least one sequence selected from:
XX CC AAY91886-903 or AAY91904-06. The preferred 12 consecutive amino acid
XX segment is chosen from AAY91907-18 or AAY91919-21. IL-1-zeta is likely to
XX play a role in systemic inflammatory reactions, such as fever,
XX hypoglycemia, reduced plasma iron and zinc, the acute response of the
XX liver, and increase plasma copper. IL-1-zeta binding compounds
XX (comprising antigen binding sites) and IL-1-zeta polypeptides are also
XX useful for both diagnostic and therapeutic purposes
XX
XX Sequence 218 AA;
SQ
Query Match 84.5%; Score 895; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 PKYKNLNPKKFSIHDDHKVLYLDSGNLAVPDKNYIRPEIFALASSLSASAEKGSPI 94
DB 50 PKYKNLNPKKFSIHDDHKVLYLDSGNLAVPDKNYIRPEIFALASSLSASAEKGSPI 109
QY 95 LLAGVSKGEFCLYCDKXGSHPSLQLKKEKMLAAQKESARRPFIYRAQVGSMMNLES 154
DB 110 LLAGVSKGEFCLYCDKXGSHPSLQLKKEKMLAAQKESARRPFIYRAQVGSMMNLES 169
QY 155 AAHPGFICTSCNCPNPGVGTDFENRKHIEFSFQPCAKEMSPSEVSD 203
DB 170 AAHPGFICTSCNCPNPGVGTDFENRKHIEFSFQPCAKEMSPSEVSD 218

```

RESULT 8
AA95299 standard; protein; 218 AA.
ID AAY95299;
AC AAY95299;
XX
XX 12-SEP-2000 (first entry)
DE Human interleukin-1 zeta splice variant TDZ.1.
XX
XX
XX Interleukin-1 zeta, IL-1 zeta, splice variant; human; TDZ.1;
XX testis-derived zeta variant; therapy; inflammation; fever.
XX Homo sapiens.
OS
XX MO200036108-A2.
PN
XX 22-JUN-2000.
PD
XX 14-DEC-1999; 99WO-US029549.
PF
XX 14-DEC-1998; 98US-0112163P.
PR 10-NOV-1999; 99US-0164675P.
XX
XX (IMMV) IMMUNEX CORP.
PA
PI Sims JE, Smith DE, Born TL;
DR WPI, 2000-442387/38.
XX N-PSDB; AAA27920.
XX
XX
XX Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and insulin-
PT dependent diabetes mellitus.
XX
XX
XX Claim 10; Page 11; 87pp; English.

The present sequence is that of splice variant TDZ.1 (testis-derived zeta variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.1 mRNA is generated from exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus, and the encoded protein is probably a functional IL-1 like molecule. TDZ.1 mRNA is expressed most strongly in the kidney, skeletal muscle, testis, prostate, ovary, colon, small intestine, liver, placenta, lung, tonsil, foetal liver, lymph node and bone marrow. The invention is directed to novel, purified and isolated IL-1 zeta, its splice variants and Xrec2 polypeptides (see AAY95297-301), the nucleic acids (see AAA27918-22) encoding such polypeptides, processes for production of recombinant forms of such polypeptides, and their uses. The polypeptides can be used to study cellular processes such as immune regulation, cell proliferation, cell death, cell migration, cell-to-cell interaction and inflammatory responses, to identify proteins associated with IL-1 zeta, to screen for potential inhibitors, and to prepare antibodies. In particular, they can be used to activate and/or inhibit the activation of vascular endothelial cells and lymphocytes, induce and/or inhibit the induction of local tissue destruction and fever, inhibit and/or stimulate macrophages and vascular endothelial cells to produce IL-6, induce and/or inhibit the induction of prostaglandins, nitric oxide synthetase, and metalloproteinases, and upregulate and/or inhibit the upregulation of molecules on the surface of vascular endothelial cells

Sequence 218 AA;
SQ

Query Match 84.5%; Score 895; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVKNNPPKKFSIHDDHKVLVDGNNLJAVPDKNYIRPEIFPALASSLSASAEKGSPI 94
DB 50 PKVKNNPPKKFSIHDDHKVLVDGNNLJAVPDKNYIRPEIFPALASSLSASAEKGSPI 109
QY 95 LIGVSKGEFCLYCDKKGSHPSLQJKEKMLKLAQKESARRPFIYFAQVGSNNMLES 154

DB 110 LIGVSKGEFCLYCDKKGSHPSLQJKEKMLKLAQKESARRPFIYFAQVGSNNMLES 169
QY 155 AAHPGWFICTSCNCPVGVTDKFNKRKHIEFSPQVCAEMSPSEVSD 203
DB 170 AAHPGWFICTSCNCPVGVTDKFNKRKHIEFSPQVCAEMSPSEVSD 218

RESULT 9
AAY96940 standard; protein; 218 AA.
ID AAY96940;
AC AAY96940;
XX
XX 31-OCT-2000 (first entry)
DE Human IL-1 receptor antagonist 1 V.
XX
XX hIL-1RA1V; human interleukin-1 receptor antagonist-1; IL-1p;
XX osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
XX anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
XX anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
XX gene therapy.
OS
XX Homo sapiens.
XX
XX MO200039297-A2.
PN
XX 06-JUL-2000.
PD
XX 22-DEC-1999; 99WO-US030720.
PF
XX 23-DEC-1998; 98US-0113430P.
PR 22-JAN-1999; 99US-0116843P.
PR 13-APR-1999; 99US-0129122P.
XX
XX (GETH) GENENTECH INC.
PA
PI Goddard A, Pan J;
DR WPI, 2000-452395/39.
XX N-PSDB; AAA51604.
XX
XX Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT preventing and treating e.g. inflammation, asthma and psoriasis.
PT
XX Claim 22; Fig 19; 143pp; English.

An isolated nucleic acid molecule encoding an interleukin-1-like polypeptide (IL-1lp) that retains one or more activities of the peptide from which it is derived, such as the IL-18R binding activity of a human interleukin-1 receptor antagonist-1 (hIL-1RA1) polypeptide, is new. The nucleic acids may be used in molecular engineering applications, e.g. hybridization assays and chromosome and gene mapping studies, for recombinantly producing the IL-1lp polypeptide or for producing gene knock out animals to study the role of the protein in metabolism and disease processes (conversely, gene therapy protocols may be used to supplement a patient's production of the polypeptide or to rectify mutations that lead to the production of in active peptides). The peptides produced may be used to screen for and produce modulators (e.g. antibodies) of IL-1lp protein expression and activity which may be used to treat disorders associated with inappropriate IL-1lp expression and activity, such as inflammatory disorders, asthma, arthritis, osteoarthritis, sepsis, acute lung injury, adult respiratory distress syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease, psoriasis, graft versus host disease and/or inflammatory bowel disease

Sequence 218 AA;
SQ

Query Match 84.5%; Score 895; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 35 PKVKNLPPKFSIHDDHKVLVLDGSLIAPDPKNYIRPEIFPALASSLSASAEKGSPI 94
Db 50 PKVKNLPPKFSIHDDHKVLVLDGSLIAPDPKNYIRPEIFPALASSLSASAEKGSPI 109
Oy 95 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSNNLES 154
Db 110 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSNNLES 169
Oy 155 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPQVCKAEMSPSEVSD 203
Db 170 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPQVCKAEMSPSEVSD 218

RESULT 10
AAB28266
ID AAB28266 standard; protein; 218 AA.
XX
AC AAB28266;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human interleukin-1 homologue IL-1H4.
XX
KM Human; interleukin-1 homologue; IL-1H4; inflammation; septicemia;
KM autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;
KM transplant rejection; graft versus host disease; infection; stroke;
KM ischaemia; acute respiratory disease; allergy; asthma; restenosis;
KM brain injury; AIDS; bone disease; osteoporosis; cancer;
KM congestive heart failure; atherosclerosis; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN MO200063226-A1.
XX
PD 26-OCT-2000.
XX
PF 14-APR-2000; 2000WO-US010207.
XX
PR 16-APR-1999; 99US-00293625.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Young PR. McDonnell PC;
XX
DR WPI; 2000-687155/67.
XX
DR N-PSDB; AAC66727.
XX
PT Interleukin-1 homolog useful for treating conditions such as chronic and
PT acute inflammation, septicemia, autoimmune diseases ischemia, acute
PT respiratory disease, allergies, and asthma.
XX
PS Claim 1; Page 28-29; 30pp; English.
XX
CC The present sequence is human interleukin-1 homologue (IL-1H4). IL-1H4 is
CC useful for treating conditions such as chronic and acute inflammation,
CC septicemia, autoimmune diseases (e.g. inflammatory bowel disease,
CC psoriasis, and arthritis), transplant rejection, graft versus host
CC disease, infection, stroke, ischaemia, acute respiratory disease,
CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.
CC osteoporosis), cancer, congestive heart failure, atherosclerosis, and
CC Alzheimer's disease, related to either an excess of, or an under-
CC expression of, IL-1H4 polypeptide activity
XX
SQ Sequence 218 AA;
Oy Query Match 84.5%; Score 895; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 35 PKVKNLPPKFSIHDDHKVLVLDGSLIAPDPKNYIRPEIFPALASSLSASAEKGSPI 94
Db 50 PKVKNLPPKFSIHDDHKVLVLDGSLIAPDPKNYIRPEIFPALASSLSASAEKGSPI 109

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Oy 95 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSNNLES 154
Db 110 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSNNLES 169
Oy 155 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPQVCKAEMSPSEVSD 203
Db 170 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPQVCKAEMSPSEVSD 218

RESULT 11
AAB47186
ID AAB47186 standard; protein; 218 AA.
XX
AC AAB47186;
XX
DT 29-JUN-2001 (first entry)
XX
DE IL-1 related polypeptide.
XX
KM Interleukin-1-related polypeptide; HPB-MLT cell; T-cell; inhibition;
KM natural killer activity; immune system; gene therapy; immunodeficiency.
XX
OS Homo sapiens.
XX
PN EP1092773-A2.
XX
PD 18-APR-2001.
XX
PF 11-OCT-2000; 2000EP-00308948.
XX
PR 15-OCT-1999; 99JP-00294493.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Ushio S, Mukada Y, Yamamoto K, Kurimoto M;
XX
DR WPI; 2001-275206/29.
XX
DR N-PSDB; AAC65680.
XX
PT New human interleukin-1-related polypeptide and polynucleotide, useful
PT for gene therapy and in developing drugs as regulators of natural killer
PT activity, are capable of inhibiting natural killer activity.
XX
PS Claim 1; Page 12; 15pp; English.
XX
CC This sequence represents an interleukin-1 (IL-1)-related polypeptide. IL-
CC 1 related polypeptide was isolated from HPB-MLT cells, FERM-BP-2430, an
CC established human T-cell line. IL-1 related polypeptide is useful for
CC inhibiting natural killer (NK) activity, which is related to the immune
CC system of mammals. The DNA encoding the IL-1 related polypeptide is
CC useful in gene therapy of patients in need of NK activity inhibition and
CC others suffering from immunodeficiency
XX
SQ Sequence 218 AA;
Oy Query Match 84.5%; Score 895; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 35 PKVKNLPPKFSIHDDHKVLVLDGSLIAPDPKNYIRPEIFPALASSLSASAEKGSPI 94
Db 50 PKVKNLPPKFSIHDDHKVLVLDGSLIAPDPKNYIRPEIFPALASSLSASAEKGSPI 109
Oy 95 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSNNLES 154
Db 110 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSNNLES 169
Oy 155 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPQVCKAEMSPSEVSD 203
Db 170 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPQVCKAEMSPSEVSD 218

RESULT 12

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	AAG68116	ID	AAG68116 standard; protein; 218 AA.
KM	AAC	AC	AAG68116;
KM	XX	DT	22-JAN-2002 (first entry)
KM	XX	DE	Human interleukin 1 family protein SEQ ID NO:2.
KM	XX	KW	Human: interleukin 1; IL-1; growth factor; Tango-77; diagnosis; identification.
KM	XX	OS	Homo sapiens.
KM	PJ	PN	JP2001231578-A.
KM	PD	XX	28-AUG-2001.
KM	PF	XX	07-DEC-2000; 2000JP-00372864.
KM	PR	XX	09-DEC-1999; 99JP-00349780.
KM	PA	(KYOW) KYOMA HAKKO KOGYO KK.	
KM	DR	WIPI; 2001-609968/70.	
KM	N-PSDB; AAI71179.		
PT	An IL-1 family protein, used for the development of diagnostic and treatment agents.		
PS	Claim 1; Page 30; 38pp; Japanese.		
CC	The present sequence represents a human interleukin 1 (IL-1) family protein having a combining affinity to a receptor of a protein of human IL-1 family higher than Tango-77. The protein is useful for the development of diagnostic, treating and/or preventive agents for various diseases		
SQ	Sequence 218 AA;		
Query Match	84.5%; Score 895; DB 4; Length 218; Best Local Similarity 100.0%; Pred. No. 1.9e-94;		
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0,			
DG	35 PKVKNLNPKKFSIHDDHKVLVDSGNLIAPDPKNYIRPEIFPALASSLSASAEKGSP I 94		
DH	50 PKVKNLINPKKFSIHDDHKVLVDSGNLIAPDPKNYIRPEIFPALASSLSASAEKGSP I 109		
DY	95 LLGVSKGEFCYCDDKQGSHPSIQLKKEXLMLKLAOKESARRPFIFFRAOVGSNNMES 154		
DL	110 LLAGSKEGFCLYCDXDKQSHSLQLKKEXLMLKLAOKESARRPFIFFRAOVGSNNMES 169		
DZ	155 AABRGMPICTSNCNEPVGTIDKFENRKHIEFSPQVCAEMSPSEVS D 203		
DA	170 AABRGMPICTSNCNEPVGTIDKFENRKHIEFSPQVCAEMSPSEVS D 218		
RESULT 13			
AAB85136	ID	AAB85136 standard; protein; 218 AA.	
AA85136;			
22-AUG-2001	(first entry)		
Interleukin-1 homologue (IL-1H4) polypeptide.			
Interleukin-1; IL-1H4; anti-inflammatory; antibacterial; antiallergic; immunosuppressive; antipsoctic; antiatherosclerotic; cytostatic; anti-HIV; cerebroprotective; antisthmatic; vasotrophic; vulnary; osteopathic; immunostimulant; antiarteriosclerotic; nootropic; neuroprotective; gene therapy; vaccine.			

OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	/note= "signal peptide"
FT	Cleavage-site
FT	Protein
FT	/note= "specifically claimed mature protein (AAB85138) "
XX	
FN	M0200140247-A1.
XX	
PD	07-JUN-2001.
XX	
XX	30-NOV-2000; 2000WO-US032521.
PE	
PR	01-DEC-1999; 99US-00452140.
XX	
XA	(SMIK) SMITHKLINE BEECHAM CORP.
FA	
PI	Kumar S, McDonnell PC, Young PR;
XX	
DR	WPI : 2001-389949/41.
DR	N-PSTD; AAF64120.
PT	Novel interleukin-1 homolog, IL-1H4, for treating chronic and acute inflammation, septicemia, autoimmune diseases, transplant rejection, graft versus host disease, stroke, ischemia, allergy and asthma.
PS	Example; Page 29; 30pp; English.
XX	The invention provides an isolated interleukin-1 homologue, IL-1H4 polypeptide. The IL-1H4 polypeptide can be expressed by standard recombinant methodology. The IL-1H4 polypeptide, polynucleotides and modulators are useful for treating chronic and acute inflammation, septicemia, autoimmune diseases (e.g., inflammatory bowel disease, psoriasis and arthritis), transplant rejection, graft versus host disease, infection, stroke, ischemia, acute respiratory disease syndrome, allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g., osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4 polynucleotides are useful as diagnostic reagents and for chromosome identification. The present sequence represents the IL-1H4 polypeptide
SO	Sequence 218 AA;
Qy	Query Match 84.5%; Score 895; DB 4; Length 218; Best Local Similarity 100.0%; Pred. No. 1.9e-94; Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	35 PKYNLNPKKESHIDDOHKVLVLDGSLINVPDKNYIRPEIFFPLASSASAEKGSPI 94 Db 50 PKYNLNPKKESHIDDOHKVLVLDGSLIAPDPKNYIRPEIFFPLASSASAEKGSPI 109
OY	95 LLGVSKSEFCILCDKDGKSGSHPSQLTKKEKLMKLAOKESARRPFIFYRAQVGSMNMLS 154 Db 110 LLGVSKSEFCILCDKDGKSGSHPSQLTKKEKLMKLAOKESARRPFIFYRAQVGSMNMLS 169
OY	155 AAPHGMITCTISGNENEPYGVTDKRENKRHIFFSPQPVCKAEMSGSEVSVD 203 Db 170 AAPHGMITCTISGNENEPYGVTDKRENKRHIFFSPQPVCKAEMSGSEVSVD 218
RESULT 14	
ID	AA711084 standard; protein; 218 AA.
XX	
AC	AA711084;
XX	
DT	05-SEP-2000 (first entry)
XX	
DE	Human zilla4-E200D variant protein.
XX	
TW	Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;

psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
anemia; inflammatory bowel disease; acute neuropathology; shock;
chronic neuropathology; respiratory disease syndrome; restenosis;
acquired immune deficiency syndrome; AIDS; anti-inflammatory; cytostatic;
anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
anti-anaemic; neuroprotective; vasotropic; variant;
anti-human immunodeficiency virus; HIV.
XX
OS Homo sapiens.
XX
PN WO200024899-A2.
XX
PD 04-MAY-2000.
XX
PF 27-OCT-1999; 99WO-US025038.
XX
PR 27-OCT-1998; 98US-00179614.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI West RR, Sheppard PO, Gao Z;
XX
DR WPI; 2000-350740/30.
XX
PT Immunomodulatory interleukin-1 homolog zll1a4 proteins, useful for
PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT disease, leukemia.
XX
PS Claim 3; Page; 88pp; English.
XX
CC The present sequence is a variant of human interleukin (IL)-1 homolog
CC zll1a4 protein, consisting of Asp in place of Glu at position 200. The
CC replacement of Glu (200) with Asp results in attenuation of pro-
CC inflammatory activity of zll1a4 protein. The zll1a4 proteins modulate
CC inflammation and other immunological processes and are therefore useful
CC for treatment of arthritis, psoriasis, septic shock, graft-versus-host
CC disease and leukaemia. Other diseases that may be modulated by zll1a4
CC proteins include cancer, anaemia, inflammatory bowel disease, acute and
CC chronic neuropathologies, shock, respiratory disease syndrome, restenosis
CC and acquired immune deficiency syndrome. Note: The present sequence is
CC not shown in the specification but is derived from human zll1a4 protein
CC sequence shown in figure-2 (AAV70927)
XX
SQ Sequence 218 AA:
Query Match 84.2%; Score 892; DB 3; Length 218;
Best Local Similarity 99.4%; Pred. No. 4.2e-94;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 35 PKVKNLPPKKESTIHDDHKVLYLDSGNLIAPDKNYIRPEIFPALASSLSASAEKSGSPI 94
DB 50 PKVKNLPPKKESTIHDDHKVLYLDSGNLIAPDKNYIRPEIFPALASSLSASAEKSGSPI 109
QY 95 LLAGVSKGEFLCYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIFRYAQVGSMMNLES 154
DB 110 LLAGVSKGEFLCYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIFRYAQVGSMMNLES 169
QY 155 AAHPGWFICTSCNENPEVGTDKFENRKHIFSFQPVCKAEMSPSEVSD 203
DB 170 AAHPGWFICTSCNENPEVGTDKFENRKHIDFSFQPVCKAEMSPSEVSD 218
RESULT 15
AAV70933
ID AAV70933 standard; protein; 218 AA.
XX
AC AAV70933;
XX
DT 05-SEP-2000 (first entry)
XX
DE Human zll1a4-E200K variant protein.
XX
KM Human interleukin-1, IL-1; zll1a4 protein; inflammation; arthritis;

psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
anemia; inflammatory bowel disease; acute neuropathology; shock;
chronic neuropathology; respiratory disease syndrome; restenosis;
acquired immune deficiency syndrome; AIDS; anti-inflammatory; cytostatic;
anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
anti-anaemic; neuroprotective; vasotropic;
anti-human immunodeficiency virus; HIV.
XX
OS Homo sapiens.
XX
PN WO200024899-A2.
XX
PD 04-MAY-2000.
XX
PF 27-OCT-1999; 99WO-US025038.
XX
PR 27-OCT-1998; 98US-00179614.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI West RR, Sheppard PO, Gao Z;
XX
DR WPI; 2000-350740/30.
DR N-PSDB; AAD00212.
XX
PT Immunomodulatory interleukin-1 homolog zll1a4 proteins, useful for
PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT disease, leukemia.
XX
PS Claim 8; Page 77-78; 88pp; English.
XX
CC The present sequence is a variant of human interleukin (IL)-1 homolog
CC zll1a4 protein designated zll1a4-E200K. The replacement of Glu (200) with
CC Lys results in change in activity from agonist to antagonist. The zll1a4
CC proteins modulate inflammation and other immunological processes and are
CC therefore useful for treatment of arthritis, psoriasis, septic shock,
CC graft-versus-host disease and leukaemia. Other diseases that may be
CC modulated by zll1a4 proteins include cancer, anaemia, inflammatory bowel
CC disease, acute and chronic neuropathologies, shock, respiratory disease
CC syndrome, restenosis and acquired immune deficiency syndrome
XX
SQ Sequence 218 AA:
Query Match 84.1%; Score 891; DB 3; Length 218;
Best Local Similarity 99.4%; Pred. No. 5.4e-94;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 35 PKVKNLPPKKESTIHDDHKVLYLDSGNLIAPDKNYIRPEIFPALASSLSASAEKSGSPI 94
DB 50 PKVKNLPPKKESTIHDDHKVLYLDSGNLIAPDKNYIRPEIFPALASSLSASAEKSGSPI 109
QY 95 LLAGVSKGEFLCYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIFRYAQVGSMMNLES 154
DB 110 LLAGVSKGEFLCYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIFRYAQVGSMMNLES 169
QY 155 AAHPGWFICTSCNENPEVGTDKFENRKHIFSFQPVCKAEMSPSEVSD 203
DB 170 AAHPGWFICTSCNENPEVGTDKFENRKHIDFSFQPVCKAEMSPSEVSD 218
Search completed: September 9, 2004, 13:25:12
Job time : 127 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:19:49 ; Search time 117 Seconds
(without alignments)
547.438 Million cell updates/sec

Title: US-09-869-566-5
Perfect score: 1059
Sequence: 1 MSALLILALVGAADVADYKID.....IEFSFQVCKAKMSEFSEVSD 203

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriaph:*
17: SP archaeaph:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	16.3	159	11	Q8CGA1
2	158.5	15.0	159	4	Q96GD6
3	152.5	14.4	267	13	Q73909
4	151	14.3	176	6	Q9BEH0
5	150	14.2	177	6	Q9GMZ4
6	148.5	14.0	272	13	Q9DDP2
7	148	14.0	177	6	Q866R8
8	145.5	13.7	272	13	Q8AXV9
9	141	13.3	176	6	Q9GKX2
10	137.5	13.0	272	13	Q9DDP3
11	136	12.8	273	13	Q7T056
12	129.5	12.2	276	13	Q57398
13	129.5	12.2	276	13	Q9PW18
14	128.5	12.1	238	13	Q8AXV8
15	128	12.1	267	6	Q29082
16	125	11.8	211	6	Q7YS41

17	120.5	11.4	599	11	Q91WP7	Q91WP7 mus musculus
18	115.5	10.9	260	13	Q8UQJ3	Q8UQJ3 oncorhynch
19	115.5	10.9	260	13	Q9YGD3	Q9YGD3 oncorhynch
20	112	10.6	266	6	Q9TKL1	Q9TKL1 tursiops tr
21	112	10.6	266	6	Q8WNR2	Q8WNR2 delphinapte
22	112	10.6	301	13	Q802S3	Q802S3 scylliorhinu
23	111.5	10.5	247	13	Q8QGM0	Q8QGM0 paraliichthy
24	109.5	10.3	246	13	Q98SG5	Q98SG5 scophthalmu
25	108	10.2	267	6	Q865X8	Q865X8 lama glama
26	107.5	10.2	302	13	Q7ZZK0	Q7ZZK0 triakis scy
27	107	10.1	72	6	Q77771	Q77771 equus caball
28	107	10.1	283	13	Q9PVZ5	Q9PVZ5 xenopus lae
29	106.5	10.1	254	13	Q9PT12	Q9PT12 oncorhynch
30	101.5	9.6	267	11	Q91ZL5	Q91ZL5 sigmodon hi
31	101	9.5	253	13	Q90W32	Q90W32 sparus aura
32	98	9.3	193	6	Q8HXR5	Q8HXR5 pan troglod
33	97.5	9.2	261	13	Q90W84	Q90W84 dicentrarch
34	94.5	8.9	269	6	Q8MKH3	Q8MKH3 salmistr sci
35	92	8.7	246	11	Q921R9	Q921R9 mus musculu
36	91	8.6	253	13	Q7ZC7	Q7ZC7 pagrus majo
37	89.5	8.5	153	4	Q43645	Q43645 homo sapien
38	88.5	8.4	152	6	Q8HXR6	Q8HXR6 macaca fasc
39	87.5	8.3	1201	16	Q7UYR6	Q7UYR6 rhodopirell
40	86.5	8.2	327	16	Q8A6K8	Q8A6K8 bacteroides
41	84.5	8.0	956	11	Q8VIG0	Q8VIG0 mus musculu
42	84	7.9	161	11	Q62161	Q62161 mus musculu
43	84	7.9	246	11	Q9ROT7	Q9ROT7 mus musculu
44	83.5	7.9	776	3	Q99287	Q99287 saccharomyc
45	83	7.8	246	11	Q9QUK9	Q9QUK9 mus musculu

ALIGNMENTS

RESULT 1

ID	Q8CGA1	PRELIMINARY;	PRT;	159 AA.
AC	Q8CGA1			
DT	01-MAR-2003	(TREMBLrel. 23, Created)		
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Interleukin 1 receptor antagonist.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N;			
RA	Strauberg R;			
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC042532; AAK42532.1; -			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0006955; P:immune response; IEA.			
DR	InterPro; IPR008996; Cytok_IL1_Like.			
DR	InterPro; IPR000975; Interleukin_1.			
DR	Pfam; PF00340; IL1; 1.			
DR	ProDom; PD002536; Interleukin_1; 1.			
DR	SMART; SM00125; IL1; 1.			
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.			
KW	Receptor.			
SO	SEQUENCE 159 AA; 17995 MW; BCA081C172903367 CRC64;			

Query Match

Best Local Similarity 37.1%; Score 173; DB 11; Length 159;
Matches 53; Conservative 25; Mismatches 75; Indels 12; Gaps 7;

Qy	27	ANSLACRGPVKYNINPKKFSIHDDHRYLVDSGNLIAVDPKNYIR-PEIFPALASSISS 85
Db	2	ASEAACRPSGRPCQKMAFRIMDTNQTFFYLRNNQLIA---GYLQSPNI--KLEEKLD 55

QY		86	ASAKGSGPILLGVSGEEFCVCDKXGSHPSLQJKEKIMTKLAQKSARPPFIYFAQ	145
Dd		56	VPIDLHS-VELGIHGCKCLCSAAGSDDI--KLQLEEVNTDLSKQEKDRK-FPIIRSE	111
QY		146	VGSMMMLESAHPGWFICTSCNCPNPVGTDFENRKHI-EFSFQ	189
Dd		112	KGPFTSPESAACPGMFLCTTLEADRPVLNTINPEEPPLIVTKRYFQ	156
 RESULT 2				
ID	Q96GD6		PRELIMINARY;	PRT; 159 AA.
AC	O96GD6:			
DT	01-DEC-2001	(TREMBLrel. 19,	Created)	
DT	01-DEC-2001	(TREMBLrel. 19,	Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)	
DE	Interleukin 1 receptor antagonist.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pancreas;			
RA	Strauberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; BC009745; AAA09745.1; -			
DR	PIR; I37893; A39386.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0006955; P:immune response; IEA.			
DR	InterPro; IPR008996; CytoC_IL1_like.			
DR	InterPro; IPR000975; Interleukin_1.			
DR	Pfam; PF00340; IL1; 1.			
DR	ProDom; PD002536; Interleukin_1; 1.			
DR	SMART; SM0125; IL1; 1.			
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.			
KW	Receptor.			
SQ	SEQUENCE 159 AA; 17888 MW; CID6CDFOD2F7B44 CRC64;			
 Query Match 15.0%; Score 158.5; DB 4; Length 159; Best Local Similarity 29.1%; Pred. No. 5.6e-08; Matches 44; Conservative 29; Mismatches 67; Indels 11; Gaps 6				
QY		27	ANSALCRGPKYNLNPFKFSIHDDPHKYLVDSGNLIWPDKNYR-DEIFPALASSISS	85
Dd		2	ALETICRSGSKSSSMQAFRIMDVNQKTFYLRRNLVA---GYIGPNV-NLEEKIDV	55
QY		86	ASAERKGSBILLGVSGEFCVCDKXGSHPSLQJKEKIMTKLAQKSARPPFIYFAQ	145
Dd		56	VPIPHA-LFIGIHGCKMCLCSVSGDETR--LQLAEAVNTDLSNRKQDKR-FAFIRS	111
QY		146	VGSMMMLESAHPGWFICTSCNCPNPVGTDFENRKHI-EFSFQ	189
Dd		112	SGPTTSFESAACPGMFLCTTLEADRPVLNTINPEEPPLIVTKRYFQ	156
 RESULT 3				
ID	Q73909		PRELIMINARY;	PRT; 267 AA.
AC	O73909:			
DT	01-AUG-1998	(TREMBLrel. 07,	Created)	
DT	01-AUG-1998	(TREMBLrel. 07,	Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)	
DE	Interleukin-1BETA.			
GN	IL-1BETA OR IL1B.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aveae; Neognathae; Galliformes; Phasianidae; Phasianine;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			

RP	SEQUENCE FROM N.A.	RA	Weining K.C., Sick C., Kasper B., Staeheli P., Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases. <td>RA</td> <td>Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.</td>	RA	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RP	SEQUENCE FROM N.A. <td>RC</td> <td>STRAIN-line N;</td>	RC	STRAIN-line N;
RT	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases. <td>RA</td> <td>Kaiser P., Rothwell L., Goodchild M., Bumstead N.;</td>	RA	Kaiser P., Rothwell L., Goodchild M., Bumstead N.;
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases. <td>RT</td> <td>"Chicken interleukin-1b: an evolutionary bridge between fish and mammals";</td>	RT	"Chicken interleukin-1b: an evolutionary bridge between fish and mammals";
DR	EMBL; Y15006; CAA75239.1; - <td>RL</td> <td>Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.</td>	RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AJ245728; CAC04510.1; - <td>DR</td> <td>EMBL; Y15006; CAA75239.1; -</td>	DR	EMBL; Y15006; CAA75239.1; -
DR	HSSP; P18510; IILR. <td>DR</td> <td>EMBL; AJ245728; CAC04510.1; -</td>	DR	EMBL; AJ245728; CAC04510.1; -
DR	GO; GO:0005576; C:extracellular; IEA. <td>DR</td> <td>HSSP; P18510; IILR.</td>	DR	HSSP; P18510; IILR.
DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA. <td>DR</td> <td>GO; GO:0005576; C:extracellular; IEA.</td>	DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0006955; P:immune response; IEA. <td>DR</td> <td>GO; GO:0005149; F:interleukin-1 receptor binding; IEA.</td>	DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR	GO; GO:0006955; P:immune response; IEA. <td>DR</td> <td>GO; GO:0006955; P:immune response; IEA.</td>	DR	GO; GO:0006955; P:immune response; IEA.
DR	InterPro; IPR008996; Cytok IL1 like. <td>DR</td> <td>GO; GO:0006955; P:immune response; IEA.</td>	DR	GO; GO:0006955; P:immune response; IEA.
DR	InterPro; IPR003502; IL1_propep. <td>DR</td> <td>InterPro; IPR008996; Cytok IL1 like.</td>	DR	InterPro; IPR008996; Cytok IL1 like.
DR	InterPro; IPR000973; Interleukin_1. <td>DR</td> <td>InterPro; IPR003502; IL1_propep.</td>	DR	InterPro; IPR003502; IL1_propep.
DR	Pfam; PF00340; IL1; 1. <td>DR</td> <td>InterPro; IPR000973; Interleukin_1.</td>	DR	InterPro; IPR000973; Interleukin_1.
DR	Pfam; PF02394; IL1_propep; 1. <td>DR</td> <td>Pfam; PF00340; IL1; 1.</td>	DR	Pfam; PF00340; IL1; 1.
DR	Prodom; PD002536; Interleukin_1. <td>DR</td> <td>Pfam; PF02394; IL1_propep; 1.</td>	DR	Pfam; PF02394; IL1_propep; 1.
DR	SMART; SM00125; IL1; 1. <td>DR</td> <td>Prodom; PD002536; Interleukin_1.</td>	DR	Prodom; PD002536; Interleukin_1.
DR	PROSITE; PS00253; INTERLEUKIN_1; 1. <td>DR</td> <td>SMART; SM00125; IL1; 1.</td>	DR	SMART; SM00125; IL1; 1.
DR	PROSITE; PS00253; INTERLEUKIN_1; 1. <td>DR</td> <td>PROSITE; PS00253; INTERLEUKIN_1; 1.</td>	DR	PROSITE; PS00253; INTERLEUKIN_1; 1.
FT	CHAIN 106 267 INTERLEUKIN-1BETA. <td>DR</td> <td>PROSITE; PS00253; INTERLEUKIN_1; 1.</td>	DR	PROSITE; PS00253; INTERLEUKIN_1; 1.
SO	SEQUENCE 267 AA; 29822 MW; 35F73164B4D40B64 CRC64; <td>FT</td> <td>CHAIN 106 267 INTERLEUKIN-1BETA.</td>	FT	CHAIN 106 267 INTERLEUKIN-1BETA.
Query Match	14.4%; Score 152.5; DB 13; Length 267;	SO	SEQUENCE 267 AA; 29822 MW; 35F73164B4D40B64 CRC64;
Best Local Similarity	28.5%; Pred. No. 4.3e-07;	Query Match	14.4%; Score 152.5; DB 13; Length 267;
Matches	59; Conservative 31; Mismatches 74; Indels 43; Gaps 11;	Best Local Similarity	28.5%; Pred. No. 4.3e-07;
QY	2 SALLILALV-----GAAVADYKDDDKLAA-----ANSALCRGKVNKNPKK 44	Matches	59; Conservative 31; Mismatches 74; Indels 43; Gaps 11;
Db	59 AAVLVAMVTKLRRPRSRDPADSD--LSALLEVFEPYFQRLSSYAGAPAFRTSRQS 116	QY	2 SALLILALV-----GAAVADYKDDDKLAA-----ANSALCRGKVNKNPKK 44
QY	45 FSIHQDHQKVLVYDLS-GLNLAV-----PDKRYIPELFFALLASSLSAAKGS----- 92	Db	59 AAVLVAMVTKLRRPRSRDPADSD--LSALLEVFEPYFQRLSSYAGAPAFRTSRQS 116
Db	117 FDIPIHQKCVLSEPTQLVALHQLGSSSQKRLNI-----ALYRPRGSGAGTGQM 170	QY	45 FSIHQDHQKVLVYDLS-GLNLAV-----PDKRYIPELFFALLASSLSAAKGS----- 92
QY	93 PILGVSGKEFCLCDKDGSHPSLDLCKEKLMLKLAQKESARRPFIYFR--AQVGSWN 150	Db	117 FDIPIHQKCVLSEPTQLVALHQLGSSSQKRLNI-----ALYRPRGSGAGTGQM 170
Db	171 PVALGI-KG-YKLYMSCVMSTTEPTQLLEADVNRDIDSVLTR--PIFYLDSPTEGTT 226	QY	93 PILGVSGKEFCLCDKDGSHPSLDLCKEKLMLKLAQKESARRPFIYFR--AQVGSWN 150
QY	151 MLESAAHPGWFICTSCNCNEBPVGTDK 177	Db	171 PVALGI-KG-YKLYMSCVMSTTEPTQLLEADVNRDIDSVLTR--PIFYLDSPTEGTT 226
Db	227 RFESAAPFGWFICTSLQPRQVGTINQ 253	QY	151 MLESAAHPGWFICTSCNCNEBPVGTDK 177
RESULT 4		Db	227 RFESAAPFGWFICTSLQPRQVGTINQ 253
Q9BEHO	PRELIMINARY; PRT; 176 AA.	Q9BEHO	PRELIMINARY; PRT; 176 AA.
AC	O9BEHO;	AC	O9BEHO;
DT	01-JUN-2001 (TREMBLrel. 17, Created)	DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)	DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE	Interleukin-1 receptor antagonist.	DE	Interleukin-1 receptor antagonist.
OS	Canis familiaris (Dog).	OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Plissipedia; Canidae; Canis.	OC	Mammalia; Eutheria; Carnivora; Plissipedia; Canidae; Canis.
OX	NCBI_TaxID=9615;	OX	NCBI_TaxID=9615;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RA	Shin I.-S., Youn H.-Y.;	RA	Shin I.-S., Youn H.-Y.;
RT	"Molecular cloning of canine interleukin-1 receptor antagonist (IL-1ra)";	RT	"Molecular cloning of canine interleukin-1 receptor antagonist (IL-1ra)";
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AY026462; AA001472.1; -	RL	EMBL; AY026462; AA001472.1; -
DR	HSSP; P18510; IILR.	DR	HSSP; P18510; IILR.
DR	GO; GO:0005576; C:extracellular; IEA.	DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA.	DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.	DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0006955; P:immune response; IEA.	DR	GO; GO:0006955; P:immune response; IEA.


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DR InterPro; IPR008996; CytoC IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Receptor.
SQ SEQUENCE 176 AA; 19922 MW; 8486CA54A240212B CRC64;

Query Match 14.3%; Score 151; DB 6; Length 176;
Best Local Similarity 28.9%; Pred. No. 3.6e-07;
Matches 46; Conservative 27; Mismatches 76; Indels 10; Gaps 6;

QY 32 CRGKVKNLNPKKPSIHQDHKVLVDSGNLIAPDKNYIRPEIFPALASSLSASAKG 91
DB 25 CRPIGKPKPCRMQARIMDVNOKTLYLRNNQLVA---GYLQGS-NTKLEKLDVVPVEPH 79
QY 92 SPILLGVSKGEFCLYCDKQSHPSIQLKKEKLMKLAQKESARRPIFYRAQVGSWM 151
DB 80 A-VFLGIHGKGLCLACVKSDETR--LQLEAVNITDLSKNDQDKR-FTFILSDSGPTTS 135
QY 152 LESAAHPGWFICTSCNCPNPGVTDKFNRRKH- EFSFQ 189
DB 136 FESAACPGWFLCTALADRPVSLNRPPEAMVTKFYFQ 174

RESULT 5
Q9GMZ4 PRELIMINARY; PRT; 177 AA.
ID Q9GMZ4
AC Q9GMZ4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-1 receptor antagonist.
GN IL-1RA.
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Tursiops.
OC NCBI_Taxid=9739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2109087; PubMed=11182153;
RA Inoue Y., Iou T., Jimbo T., Syouji Y., Ueda K., Sakai T.;
RT "Molecular cloning and functional expression of bottle-nosed dolphin
RL (Tursiops truncatus) Interleukin-1 receptor antagonist."
Vet. Immunol. Immunopathol. 78:131-141(2001).
DR EMBL; AB038268; BAB11806.1; -.
DR HSSP; P18510; 1IRA.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:Interleukin-1 receptor binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; CytoC IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Receptor.
SQ SEQUENCE 177 AA; 19923 MW; 6FD19A06C09B131B CRC64;

Query Match 14.2%; Score 150; DB 6; Length 177;
Best Local Similarity 28.4%; Pred. No. 4.6e-07;
Matches 46; Conservative 21; Mismatches 53; Indels 42; Gaps 6;

QY 45 FSIHDOHKVLVDSGNLI-----VPDKNYIRPEIFPALASSLSASA 88
DB 38 FRIDVQKTFYLRNNQVAGYLOGPNTKLEKIDVVP---IEPHMF----- 82
QY 89 EKSPILLGVSKGEFCLYCDKQSHPSIQLKKEKLMKLAQKESARRPIFYRAQVGS 148
DB 83 -----LGIHGKGLCLACVKSDEI--KGLERVNTDLSKSKEDKR-FAFIRSDSGP 132

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QY 149 MNLESAAHPGWFICTSCNCPNPGVTDKFNRRKH- EFSFQ 189
DB 133 TTSPESAACPGWFLCTALADRPVSLNRPPEAMVTKFYFQ 174

RESULT 6
Q9DDF2 PRELIMINARY; PRT; 272 AA.
ID Q9DDF2
AC Q9DDF2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 1 beta 2-2.
GN IL-1 BETA 2.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OC NCBI_Taxid=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Engelma M.Y., Stet R.J.M., Verbarg-van Kemenade L.B.M.;
RT "Cloning and sequencing of two carp interleukin 1 beta 2 complementary
RL DNAs."
J. Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ401031; CACI9888.1; -.
DR HSSP; P01584; 211B.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:Interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR008996; CytoC IL1 like.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF00394; IL1_propep; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Receptor.
SQ SEQUENCE 272 AA; 30547 MW; C87FE9D7B6438BE4 CRC64;

Query Match 14.0%; Score 148.5; DB 13; Length 272;
Best Local Similarity 26.2%; Pred. No. 1.1e-06;
Matches 43; Conservative 30; Mismatches 66; Indels 25; Gaps 5;

QY 30 ALCRGPVKNLNPKKPSIHQDHKVLVDSGNLIAPDKNYIRPEIFPALASSLSASAE 89
DB 120 SVCDKRYKKTLYQSKNLNQLDLHKAIVLTSAGT-----IQYKQFSMMVTVSSAQON 170
QY 90 KSPILLGVSKGEFCLYCDKQSHPSIQLKKEK--LMKLAQKESARRPIFYRAQV 147
DB 171 NGQPVCCGISNSMLYIACIQ-SGSGPPVLLKKEVSGFLNITADDPNGYDLSLFRKRETG 229
QY 148 -SNMLESAAHPGWFICTSCNCPNPGVTDKFNRRKHIFSFP 190
DB 230 TAYNTFESVKYPGWFISTA-----FDDWKKEVMSQVP 261

RESULT 7
Q866R8 PRELIMINARY; PRT; 177 AA.
ID Q866R8
AC Q866R8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IL-1 receptor antagonist.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_Taxid=9541;
RN [1]
RP SEQUENCE FROM N.A.

```

RX MEDLINE=22419343; PubMed=12530978;
 RA Smith D.E., Hanna R., Friend D., Moore H., Chen H., Farese A.M.,
 RA MacVittie T.J., Virca G.D., Sims J.B.,
 RT "The Soluble Form of IL-1 Receptor Accessory Protein Enhances the
 RT Ability of Soluble Type II IL-1 Receptor to Inhibit IL-1 Action",
 RL Immunity 18:87-96(2003).
 DR EMBL; AY182332; AA024703.1; -
 DR GO; GO:000576; Extracellular; IEA.
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR008996; Cytok_IL1_Like.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 KW Receptor.
 SQ SEQUENCE 177 AA; 19892 MW; FB7938A968EF360F CRC64;

Query Match 14.0%; Score 148; DB 6; Length 177;
 Best Local Similarity 30.2%; Pred. No. 7.4e-07;
 Matches 42; Conservative 26; Mismatches 57; Indels 14; Gaps 7;
 QY 42 PKK---FSIHDDHKVLDGSLIAVPDKNYIR-PEIFPALSSLSASAEGSPILLG 97
 DB 32 PSKMGQFRIMDVNQKTFYLRNQLVA---GYLGSPNV--NLEKIDVPIEPHA-LPLG 84
 QY 98 VSKGEFCLYCDKQKQSHPSLQKKEKMLAAQKESARRPFIYPAQVSNMLESAAH 157
 DB 85 IHGKMKCLSCVSKGDETR--LQLEAVNITDLSKMKODKR-FAFVSDSGPTTSFESAC 141
 QY 158 PGWFICTSCNCPVGVTD 176
 DB 142 PGWFICTSCNCPVGVTD 160

RESULT 8
 Q8AXV9 PRELIMINARY; PRT; 272 AA.
 AC Q8AXV9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Interleukin-1 beta-1.
 GN IL-1B-1.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OC NCBI_TaxID=7957;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Wang T., Bird S., Zou J., Secombes C.J.;
 RT "Sequencing, gene organization and differential expression of two
 RT goldfish IL-1 beta genes.",
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AA419848; CAD12102.1; -
 DR GO; GO:000576; Extracellular; IEA.
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
 DR GO; GO:0006954; P:immune response; IEA.
 DR GO; GO:0006954; P:inflammatory response; IEA.
 DR InterPro; IPR008996; Cytok_IL1_Like.
 DR InterPro; IPR003502; IL1_pIropep.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR Pfam; PF02394; IL1_pIropep; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 SQ SEQUENCE 272 AA; 30721 MW; A91E57D728770E13 CRC64;

Query Match 13.7%; Score 145.5; DB 13; Length 272;

Best Local Similarity 27.4%; Pred. No. 2.3e-06;
 Matches 43; Conservative 31; Mismatches 66; Indels 17; Gaps 5;
 QY 31 LCRGPVKVNLNPKKFSIHDDHKVLDGSLIAVPDKNYIRPEIFPALSSLSASAEGK 90
 DB 121 ICDKRYKTLVQSNKLNEDLHLKAVTLISAGN-----IQYKAFSNSTYLSAPQNK 171
 QY 91 GSPILLGVSKGEFCLYCDKQKQSHPSLQKKEK-LMKLAAQKESARRPFIYPAQV- 147
 DB 172 GQPVCLAI NSNLIYACTESDGS -PILLKEVSGPLNTIKVGDQGYDLSLFFRKETG 230
 QY 148 SWNMLESAAHPGWFICTSCNCPVGV---TDKFN 180
 DB 231 AVYTFESVVKYPGWYISTAFDWERVEMIQVPTDRTN 267

RESULT 9
 Q9GKK2 PRELIMINARY; PRT; 176 AA.
 AC Q9GKK2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Interleukin-1 receptor antagonist.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21109092; PubMed=11822158;
 RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duchie S.,
 RA Bennett D.;
 RT "Cloning of canine IL-1ra, TNFR and TIMP-2",
 RT Vet. Immunol. Immunopathol. 78:207-214(2001).
 RL Vec. Immunol. Immunopathol. 78:207-214(2001).
 DR EMBL; AF216526; AAG36777.1; -
 DR HSSP; P18510; IL1R.
 DR GO; GO:000576; Extracellular; IEA.
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008996; Cytok_IL1_Like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 KW Receptor.
 SQ SEQUENCE 176 AA; 19938 MW; 8486CA54A254206B CRC64;

Query Match 13.3%; Score 141; DB 6; Length 176;
 Best Local Similarity 28.3%; Pred. No. 3.7e-06;
 Matches 45; Conservative 27; Mismatches 77; Indels 10; Gaps 6;
 QY 32 CRGPVKVNLNPKKFSIHDDHKVLDGSLIAVPDKNYIRPEIFPALSSLSASAEGK 91
 DB 25 CRPLGRPCRMQAFRIWDVNOKTFYLRNQLVA---GYLGSP-NYTKLEKLDVVEPH 79
 QY 92 SPILLGVSKGEFCLYCDKQKQSHPSLQKKEKMLAAQKESARRPFIYPAQVSNM 151
 DB 80 A-VFLGIHGGKCLACVSKGDETR--LQLEAVNITDLSKMKODKR-FFIILSDSGPTTS 135
 QY 152 LESAHPGWFICTSCNCPVGVTDKFNKHI-EPSFQ 189
 DB 136 FESAACPGWFICTALADRLVSLTNRPESAMVTKRYFQ 174

RESULT 10
 Q9DDF3 PRELIMINARY; PRT; 272 AA.
 AC Q9DDF3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

	Query Match	Similarity	13.0%	Score	137.5	DB	13	Length	272;
	Best Local	Similarity	25.8%	Pred.	No. 1.5e-05				
	Matches	Conservative	42;	Mismatches	67;	Indels	25;	Gaps	5
QY	31	LGRGPKVKNLPPKKEISHDHHKVLVDLSGNLIAVPDKNRYRPEIFALASSASAEK	90						
Db	121	VCDKKTKTLVGSSNKLTNQDLHKAVTISAGT-----IYKVGFSFSPVSDPDND	171						
QY	91	GSPILLGVSKBEFCLYCDKDKGQSHPISIQLKKEK--LMKLAAQESARRPFFYYAQQVS	148						
Db	172	GQPVCGLGISNNLVIACTQ--SGGSPPVLLLEKVGSPPLNTITGDGDNGYDSLFFPKKETGT	230						
QY	149	--MNMLESAAHGPWFICTSCNCNEPVGIVDDKENRGHIESPOP	190						
Db	231	DYNTFESVKYIPGMVFISTA-----FDMDKRVESQVP	261						

Query Match	12.8%	Score 136;	DB 13;	Length 273;
Best Local Similarity	30.7%;	Pred. No. 2.1e-05;		
Matches	50;	Conservative	27;	Mismatches 70;
				Indels 16;
				Gaps 7.

RESULT	12			
057398				
ID	057398	PRELIMINARY;	PRT;	276 AA.
AC	057398;			
DT	01-JUN-1998	(TEMBLrel. 06, Created)		
DT	01-JUN-1998	(TEMBLrel. 06, Last sequence update)		
DT	01-OCT-2003	(TEMBLrel. 25, Last annotation update)		
DE	Interleukin-1 beta.			
OS	Cyprinus carpio (Common carp)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Cyprinus.			
OX	NCBI_TaxID=7962;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20394649; PubMed=10938736;			
RA	Fujiki K., Shin D.H., Nakao M., Yano T.;			
RT	"Molecular cloning and expression analysis of carp (Cyprinus carpio)			
RT	interleukin-1beta, high affinity immunoglobulin E Fc receptor gamma			
RL	subunit and serum amyloid A.";			
RL	Fish and Shellfish Immunol. 10:229-242(2000).			
DR	EMBL; AB010701; BAA24538.1; -			
DR	HSSP; P01584; IHB.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA.			
DR	GO; GO:0006855; P:immune response; IEA.			
DR	GO; GO:0006954; P:inflammatory response; IEA.			
DR	InterPro; IPR008996; Cytok_IL1_like.			
DR	InterPro; IPR003502; IL1_propep.			
DR	InterPro; IPR000975; Interleukin_1.			
DR	Pfam; PF00340; IL1_1.			
DR	Pfam; PF02394; IL1_propep; 1.			
DR	SMART; SM00125; IL1_1.			
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.			
DR	SEQUENCE 276 AA; 31070 NM; F3AC5B0A31FD07B3 CRC64;			

[illegible]

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GN IL-1.
OS Cypripus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxId=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21098506; PubMed=1164885;
RA Engelisma M.Y., Stee R.J.M., Schipper H., Verburg-van Kemnade B.M.L.;
RT "Regulation of interleukin 1 beta RNA expression in the common carp,
RT Cypripus carpio L.";
RL Dev. Comp. Immunol. 25:195-203 (2001).
DR HSSP; P01584; IHB.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR003502; IL1_propep.
DR Pfam; PF00340; IL1_1.
DR Pfam; PF02394; IL1_propep; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ SEQUENCE 276 AA; 31098 MW; 4AE31E2564A97C6A CRC64;

Query Match 12.2%; Score 129.5; DB 13; Length 276;
Best Local Similarity 23.2%; Pred. No. 9,7e-05;
Matches 38; Conservative 34; Mismatches 69; Indels 23; Gaps 4;

QY 31 LCRGPVKNLNPKKFSIHDDHKLVLVDSGNLJAVFDKNYRPEIFPALASLSASAER 90
DB 123 ICKYKKTWQSKLSDPEHLKAVLSAGAM-----QYKQFSMTFSSATQKE 173
QY 91 GSPILLGVSKGEFLCYCDKDGQSHPSLQKKEKMKLAQKESARRPFIYRAQVGS-W 149
DB 174 AQVCCIGISNSNLYLACTQDGS -PVLILKEASGVNTIKADPDNSLLFFRKETGRY 232
QY 150 NMLESAHPGWFCTSCNCEPVGVDKFNKRKHIEFSFPVCK 193
DB 233 NTFESVYKPGWFISTA-----FDMWEKVENQMPTR 264

RESULT 14
ID 08AXV8 PRELIMINARY; PRT; 238 AA.
AC 08AXV8;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Interleukin-1 beta-2.
GN IL-1B-2.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxId=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RC Wang T., Bird S., Zou J., Secombes C.T.;
RT "Sequencing, gene organisation and differential expression of two
RT goldfish IL-1 beta genes.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; A419849; CAD12103.1; -.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR003502; IL1_propep.

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DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 238 AA; 27076 MW; 71BCCL1719B7DFB07 CRC64;

Query Match 12.1%; Score 128.5; DB 13; Length 238;
Best Local Similarity 24.8%; Pred. No. 0.0001;
Matches 35; Conservative 31; Mismatches 50; Indels 25; Gaps 5;

QY 53 KYLVVDSGNLJAVPDKNYRPEIFPALASLSASAERKSPILLGVSKGEFLCYCDKDG 112
DB 103 KAVTISAGTM-----QYKQFSMTYISSATPKAQVCLISNSNLYLACTQSDG 153
QY 113 OSHPSLQKKEK-LMKLAQKESARRPFIYRAQVGS-SMNMLESAHPGWFCTSCN 169
DB 154 SS-PALILKEVGPPLNTITDDPDNGDSLLFFRKETGTAVNPFESVKPFGWFIITTA----- 208
QY 170 EPVGVTDKFNKRKHIEFSFP 190
DB 209 -----FDMWEKVENQMP 221

RESULT 15
ID 029082 PRELIMINARY; PRT; 267 AA.
AC 029082;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Interleukin 1-beta.
GN INTERLEUKIN 1-BETA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RC Vanderbroeck K.;
RA Vanderbroeck K.;
RT Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
AC 029082;
RC TISSUE=Liver;
RX MEDLINE=94039070; PubMed=8223584;
RA Vanderbroeck K., Fiten P., Beuken E., Martens E., Janssen A.,
RA Van Damme J., Opdenacker G., Billiau A.;
RT "Gene sequence, cDNA construction, expression in Escherichia coli and
RT genetically approached purification of porcine interleukin-1beta.";
RL Eur. J. Biochem. 217:45-52(1993).
DR EMBL; X74568; CAA52660.1; -.
DR PIR; S38373; S38373.
DR HSSP; P01584; IHB.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ SEQUENCE 267 AA; 29893 MW; 4830645DA5FF9967 CRC64;

Query Match 12.1%; Score 128; DB 6; Length 267;
Best Local Similarity 28.9%; Pred. No. 0.00013;
Matches 43; Conservative 28; Mismatches 66; Indels 12; Gaps 6;

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QY 27 ANSALCRGPKVKNLNPKKFSIHODHKVVLDSGNLAVPD-KNYIRPEIFPALLASSLS 84
Db 107 ANGFLCDATPVQSVDC--LQDKDEKALVLAGPHELKALHLKQDLKREVVFCMSFYQG 163
QY 85 SASAEKSPILLGVSKGEFCLYC-DKDKGQSHPSIQKKEKMLAOKESARRPFIYR 143
Db 164 DSDSDK-IPVTLGIGKKNLYLSCVWKD--DTPTLQ--EDVDPKSYPKRDMERFVFX 217
QY 144 AOVGSMNMLESAHPGWFICTSCNCEPV 172
Db 218 TEIGNRVFESALYFNNYISTQAQKPV 246

Search completed: September 9, 2004, 13:27:43
Job time : 120 secs

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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:12:44 ; Search time 23 Seconds
(without alignments)
459.576 Million cell updates/sec

Title: US-09-869-566-5
Perfect score: 1059
Sequence: 1 MSALLITALVCAAVADYKD.....IEFSFQPCVKAEMSPSEVSD 203

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	895	84.5	218	1 IF7_HUMAN	Q9NZH6 homo sapien
2	229.5	21.7	169	1 IF9_HUMAN	Q9NZH8 homo sapien
3	209	19.7	158	1 IF6_HUMAN	Q9NHA7 homo sapien
4	199	18.8	183	1 IF8_MOUSE	Q946Z6 mus musculu
5	191.5	18.1	156	1 IF5_MOUSE	Q9QY71 mus musculu
6	174.5	16.5	155	1 IF5_HUMAN	Q9BHD0 h interleuk
7	174.5	16.5	164	1 IF9_MOUSE	Q9B460 mus musculu
8	171	16.1	160	1 IF6_MOUSE	Q911A2 mus musculu
9	167	15.8	178	1 IF4_MOUSE	P25085 mus musculu
10	165.5	15.6	152	1 IF4_MOUSE	Q87459 mus musculu
11	158.5	15.0	177	1 IF4_HUMAN	P18510 homo sapien
12	156.5	14.8	152	1 IF4_HUMAN	Q8W821 homo sapien
13	154.5	14.6	177	1 IF4_MOUSE	P26890 oryctolagus
14	152	14.4	174	1 IF4_BOVIN	O77482 bos taurus
15	151	14.3	176	1 IF4_CANFA	Q9BHD0 canis famli
16	150	14.2	177	1 IF4_MOUSE	Q9BHD0 canis famli
17	146.5	13.8	177	1 IF4_MOUSE	Q9BHD0 canis famli
18	146.5	13.8	178	1 IF4_MOUSE	Q9BHD0 canis famli
19	146.5	13.8	177	1 IF4_MOUSE	Q9BHD0 canis famli
20	141.5	12.4	266	1 IF4_MOUSE	Q9BHD0 canis famli
21	141.5	11.5	267	1 IF4_MOUSE	Q9BHD0 canis famli
22	141.5	11.4	268	1 IF4_MOUSE	Q9BHD0 canis famli
23	140.5	11.4	269	1 IF4_MOUSE	Q9BHD0 canis famli
24	140.5	11.2	269	1 IF4_MOUSE	Q9BHD0 canis famli
25	140.5	11.1	266	1 IF4_MOUSE	Q9BHD0 canis famli
26	140.5	10.7	266	1 IF4_MOUSE	Q9BHD0 canis famli
27	140.5	10.0	266	1 IF4_MOUSE	Q9BHD0 canis famli
28	101	9.5	269	1 IF4_MOUSE	Q9BHD0 canis famli
29	99	9.3	268	1 IF4_MOUSE	Q9BHD0 canis famli
30	98.5	9.3	269	1 IF4_MOUSE	Q9BHD0 canis famli
31	98	9.3	269	1 IF4_MOUSE	Q9BHD0 canis famli
32	95.5	9.0	246	1 IF4_MOUSE	Q9BHD0 canis famli
33	92.5	8.7	268	1 IF4_MOUSE	Q9BHD0 canis famli

34	91	8.6	404	1 KTR3_YEAST	P38130 saccharomyc
35	89.5	8.5	267	1 IL1B_FELCA	P16877 felis silve
36	89	8.4	269	1 IL1B_MACNE	P1493 macaca neme
37	88.5	8.4	269	1 IL1B_CERTO	P16648 cercopithec
38	88.5	8.4	269	1 IL1B_XENMU	P48090 macaca mlla
39	88	8.3	473	1 MDM2_XENLA	P56273 xenopus lae
40	84	7.9	270	1 IL1A_MOUSE	P15882 mus musculu
41	83.5	7.9	269	1 IL1B_MOUSE	P79182 macaca fasc
42	82.5	7.8	246	1 TRY1_RAT	P00762 rattus norv
43	81	7.6	320	1 MOA_CAMJE	Q9P165 campyllobact
44	81	7.6	1058	1 U202_ARATH	Q9XIK4 arabidopsis
45	80.5	7.6	246	1 TRY2_RAT	P00763 rattus norv

ALIGNMENTS

RESULT 1
ID IF7_HUMAN STANDARD; PRT: 218 AA.
AC Q9NZH6; Q8TD04; Q8TD05; Q9HBR2; Q9HBP3; Q9HBA6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin 1 family member 7 precursor (IL-1F7) (Interleukin-1 zeta)
DE (IL-1 zeta) (Fili zeta) (Interleukin-1 homolog 4) (IL-1H4)
DE (Interleukin-1-related protein) (IL-1R1) (IL-1X protein).
GN IL1F7 OR FIL1Z OR IL1H4 OR IL1R1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Fetal B-cell, Fetal colon, Fetal lung, and Fetal testis;
RA MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tamas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
the Interleukin-1 family";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Colon carcinoma;
RA Manoj P.P., Mantovani A., Muzio M.;
RN Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C), SEQUENCE OF 46-54, AND VARIANTS
VAL-31 AND ALA-42.
RX MEDLINE=2106552; PubMed=1145836;
RA Pan G., Risse P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
RA Yansuata D., Lewis L., Eigenbrodt C., Henzel W.J., Vanden R.;
RT "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
1R1P";
RL Cytokine 13:1-7(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
RT "Four new members expand the IL-1 superfamily";
RL J. Biol. Chem. 275:11659-1175(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS D AND E).
RX MEDLINE=21988051; PubMed=11991723;
RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;
RT "Genomic organization of the interleukin-1 locus";
RN Genomics 79:726-733(2002).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS VAL-31 AND ALA-42.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;


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RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318623; PubMed=10860666;
RA Bufield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
RT "Identification and gene organization of three novel members of the
RT IL-1 family on human chromosome 2.";
RL Genomics 66:213-216(2000).
CC
CC -1- FUNCTION: Function as an agonist of NF-kappa B activation through
CC the orphan IL-1-receptor-related protein 2. Could constitute part
CC of an independent signaling system analogous to interleukin-1
CC alpha (IL-1a), beta (IL-1b) receptor agonist and interleukin-1
CC receptor type 1 (IL-1R1), that is present in epithelial barriers
CC and takes part in local inflammatory response.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highly expressed in tissues containing
CC epithelial cells: skin, lung, stomach and esophagus. In skin is
CC expressed only in keratinocytes but not in fibroblasts,
CC endothelial cells or melanocytes. Up-regulated in lesional
CC psoriasis skin.
CC -1- INDUCTION: By TNF-alpha and by IFN-gamma in keratinocytes.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF200492; AAF69248.1; -
DR EMBL: AF206696; AAG35670.1; -
DR HSSP: P18510; IL1F6.
DR Genew: HGNC:15741; IL1F9.
DR MIM: 605542; -
DR GO: GO:0007267; P:cell-cell signaling; TAS.
DR GO: GO:0009613; P:response to pest/pathogen/parasite; TAS.
DR InterPro: IPR008996; CytoK_IL1like.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; FALSE_NEG.
DR CytoKine; Multigene family.
KW SEQUENCE 169 AA; 18721 MW; F00A9243706FA154 CRC64;
SQ
Query March 21.7%; Score 229.5; DB 1; Length 169;
Best Local Similarity 35.0%; Pred. No. 1.2e-14;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;
QY 19 DDDDKLAANASALCRGPKVKNLNPKEFSIHDDQHKVLVLDGSLIAYDPKNYIRPEIFFA 78
DB 7 DADGGRVAVQSMCK-----PITGINDLNQOVWTLGQNLVAVDRSSVTPVAV 58
QY 79 LASSLSASAE-KSPILIGVSKGFCYCKDKGQSHPSIQLKKEKMLKLAQKESARR 137
DB 59 ITCKYPALLEGGRDPYILGIQNPEMCLYCKEVEQ--PTIQLEKQIMDLYGQPEPV-K 115
QY 138 PFIFYRAOVGSMMNLESAAHPGFICTSCNCEPVGVTDK 177
DB 116 PFLFYRAKTKRTSLTESVAFPPDWFIASS-KRDPILITSE 154
RESULT 3
ID IL1F6 HUMAN STANDARD; PRT; 158 AA.
AC OSURH7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Interleukin 1 family member 6 (IL-1F6) (Interleukin-1 epsilon) (IL-
DE 1 epsilon) (P1L1 epsilon).

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GN IL1F6 OR IL1E OR F1L1E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Kenschaw B.R., Ketchum R.R., Kudin M., Garika K.E.,
RA Sims J.E.;
RT "Four new members expand the IL-1 superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in immune system and fetal brain,
CC but not in other tissues tested or in multiple hematopoietic cell
CC lines.
CC -1- MISCELLANEOUS: Binding analysis failed to detect interaction with
CC multiple IL1R family members.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF201831; AAF25211.1; -
DR HSSP: P18510; IL1R.
DR Genew: HGNC:15562; IL1F6.
DR MIM: 605509; -
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0005149; F:interleukin-1 receptor binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR008996; CytoK_IL1like.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; FALSE_NEG.
DR CytoKine; Multigene family.
KW SEQUENCE 158 AA; 17684 MW; 469AC84306BDE280 CRC64;
SQ
Query March 19.7%; Score 209; DB 1; Length 158;
Best Local Similarity 36.7%; Pred. No. 9.3e-13;
Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;
QY 42 PKKSHDDQHKVLVLDGSLIAYDPKNYIRPEIFFLAS--SLSSASAEKGSPIILIGVS 99
DB 10 PQQGSIDINHRVWVLDQDTLIIVPRDRMSF-VTALLISCRHETLEKRGNGIYIGLN 68
QY 100 KGEFCLCDDDKGSHPSIQLKKEKMLKLAQKESARPFIFYRAOVGSMMNLESAAHPG 159
DB 69 GAINCLMCARVGD--PTIQLEKQIMDLYNQPEPV-KSLFLFHSQSGRSTFSSVAFPG 125
QY 160 WFICTSCNCEPVGVTDKFENRHHIEF 186
DB 126 WFIIVSSEGGCPILITQELKANTTDF 152
RESULT 4
ID IL1F8 MOUSE STANDARD; PRT; 183 AA.
AC OSD6Z6; OSR461;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin 1 family member 8 (IL-1F8).
GN IL1F8 OR F1L1E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

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OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster / NIH;
RX MEDLINE=21988051; PubMed=11991723;
RA Taylor S.L., Ranshaw B.R., Garke K.E., Smith D.E., Sims J.E.;
RT "Genomic organization of the interleukin-1 locus.";
RN Genomics 79:726-733 (2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hasegawa Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
CC - SUBCELLULAR LOCATION: Secreted (Potential).
CC - SIMILARITY: Belongs to the IL-1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AY071842; AAL67152.1; ALT_INIT.
CC EMBL: AK009787; BAB26505.1; -.
CC InterPro: IPR008996; CytoC_IL1_like.
CC InterPro: IPR000975; Interleukin_1.
CC MGD: MGI:1916927; IL1f8.
CC Pfam: PF00340; IL1; 1.
CC ProDom: PD002536; Interleukin_1; 1.
CC SMART: SM00125; IL1; 1.
CC PROSITE: PS00253; INTERLEUKIN_1; 1.
CC Cytokine; Multigene family.
CC KW SEQUENCE 183 AA; 20878 MW; A3ACE339FB96F02F CRC64;
SQ
Query Match 18.8%; Score 199; DB 1; Length 183;
Best Local Similarity 33.3%; Pred. No. 9.8e-12;
Matches 42; Conservative 27; Mismatches 53; Indels 4; Gaps 3;
QY 41. NPKKFSIHDDHKLVDLSGNLAVPDKNYIRPEIFPALA-SSLSASAEKSGPILIGVS 99
DB 34 SPNNRYRHDSQGMWVLTGNTLTAVPASNNVKKPITLSLINCRRDEPDKKNLVFGLIK 93
QY 100 KGEFCLYCDKDGKQSHPSLDIKKEKMLKLAQKESARPPITFRAYGVSNMMLSAHPG 159
DB 94 NNNLCFCFCVMEGR--PTLQKEVDINMLYKERK-AQKAFLEFYGIEGSTVSQSVLYPG 150
QY 160 WPICTS 165
DB 151 WPIATS 156

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ID ILF5_MOUSE
AC 090YI1; Q9JIG2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin 1 family member 5 (IL-1F5) (interleukin-1 delta (IL-1
DE delta) (interleukin-1-like protein-1) (interleukin-1-like protein 1)
DE (IL-1L1) (interleukin-1 HYL) (IL-1HYL) (interleukin-1 homolog 3) (IL-
DE 1H3).
GN ILF5 OR IL1D OR IL1H1 OR IL1H3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359532; PubMed=1146363;
RA Debers R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
RA Kastlein R.A.;
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
RT as an antagonist and agonist of NF-kappa B activation through the
RT orphan IL-1 receptor-related protein 2.";
RL J. Immunol. 167:1440-1446(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20545522; PubMed=11093146;
RA Barton J.L., Herbst R., Bosisto D., Higgins L., Nicklin M.J.H.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RL Eur. J. Immunol. 30:3299-3308(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hasegawa Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
CC - FUNCTION: Is a highly and a specific antagonist of the IL-1
CC receptor-related protein 2-mediated response to interleukin 1
CC family member 9 (IL1F9). Could constitute part of an independent
CC signaling system analogous to interleukin-1 alpha (IL-1A), beta
CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
CC 1RI), that is present in epithelial barriers and takes part in
CC local inflammatory response (By similarity).
CC - SUBCELLULAR LOCATION: Secreted (By similarity).

```

```

CC -1- TISSUE SPECIFICITY: Highly abundant in embryonic tissue and
CC tissues containing epithelial cells.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC or send an email to license@isb-sb.ch).
CC -----
DR EMBL, AF230378; AAF91275.1; -
DR EMBL, AK009741; BAB26471.1; -
DR EMBL, AK008977; BAB26002.1; -
DR EMBL, AJ250429; CAB59831.1; ALT_INIT.
DR EMBL, AF200495; AAF69251.1; -
DR HSSP; P18510; IL1R.
DR MGI; MGI:1859325; IL1F5.
DR InterPro; IPR008996; CytoK_IL1_like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR CytoKine; MultiGene family.
DR KMW CONFLICT 2 MISSING (IN REF. 3).
DR FT SEQUENCE 156 AA; 17136 MW; AAD1EE2F93CF77A7 CRC64;
SQ
Query Match 18.1%; Score 191.5; DB 1; Length 156;
Match Local Similarity 35.1%; Pred. No. 4.2e-11;
Matches 53; Conservative 24; NonMatches 51; Indels 23; Gaps 6;
QY 28 NSALCRGRKVKVNLNPKKFSIHDOHDKVLYLDSGNLIA--VPDKNYRPEIFFALASSLSS 85
Db 5 SGALC-----FRMDSAKVLYLNNQLLAGLAERKIKGEELISVFNRLD 52
QY 86 ASAEKGSPIILLGVSKGEFCLYCDKDGSGHPSLQJKEKELMKL-AAOKESARRPFIYRA 144
Db 53 ASL---SPVILGVGGSGQLSCGTEKG--PIKLKEPNIWELVYGAKE--KSPTFYRR 104
QY 145 QVGSNMMLESAARPGWFICTSCNCNEPQVGT 175
Db 105 DMGLTSSPESAAYPGWFLCTSPEDAQPVRLT 135
RESULT 6
IL1F5_HUMAN STANDARD; PRT; 155 AA.
ID IL1F5_HUMAN
AC Q9UBH0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin 1 family member 5 (IL-1F5) (interleukin-1 delta) (IL-1
DE delta) (IL1 delta) (interleukin-1-like protein 1) (IL-1L1)
DE (interleukin-1 H1) (IL-1H1) (interleukin-1 receptor antagonist
DE homolog 1) (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3).
GN IL1F5 OR IL1D OR IL1H1 OR IL1L1 OR IL1RP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta; PubMed=10625660;
RX Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
RA Sline J.E.;
RT "Four new members expand the IL-1 superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=fetal skin;
RC

```

RX MEDLINE=999443727; PubMed=10512743;
 RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
 RA Drmanac R., Ford Y.B.;
 RT "IL11R1: a novel interleukin-1 receptor antagonist gene.";
 RL Biochem. Biophys. Res. Commun. 263:702-706(1999).
 [3].
 RN SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RC MEDLINE=21359532; PubMed=11093146;
 RX Barton J.L., Herbst R., Bosisto D., Higgins L., Nicklin M.J.H.;
 RA "A tissue specific IL-1 receptor antagonist homolog from the IL-1
 RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities";
 RL Eur. J. Immunol. 30:3259-3308(2000).
 [4].
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21359532; PubMed=11466363;
 RX Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
 RA Wagner J., Edwards G., Clifford T., Memon S., Bazan J.F.,
 RA Kastelein R.A.;
 RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
 RT as an antagonist and agonist of NF-kappa B activation through the
 RT orphan IL-1 receptor-related protein 2.";
 RL J. Immunol. 167:1440-1446(2001).
 [5].
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20318623; PubMed=10860666;
 RX Busfield S.J., Comstock C.A., Yu G., Chickering T.W., Smutko J.S.,
 RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
 RT "Identification and gene organization of three novel members of the
 RT IL-1 family on human chromosome 2.";
 RL Genomics 66:213-216(2000).
 [6].
 RN SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuller G.D.,
 RA Ahschl S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stetson M., Soares B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loughlan N.A., Peters G.J., Adomson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanev J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:116899-16903(2002).
 [7].
 RN SEQUENCE FROM N.A.
 RP FUNCTION: Is a highly and a specific antagonist of the IL-1
 CC receptor-related protein 2-mediated response to interleukin 1
 CC family member 9 (IL19). Could constitute part of an independent
 CC signaling system analogous to interleukin-1 alpha (IL-1A), beta
 CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
 CC 1R1), that is present in epithelial barriers and takes part in
 CC local inflammatory response.
 CC [8].
 RN SEQUENCE FROM N.A.
 RP TISSUE SPECIFICITY: Predominantly expressed in keratinocytes but
 CC not in fibroblasts, endothelial cells or melanocytes. Detected
 CC also in the spleen, brain leukocyte and macrophage cell types.
 CC [9].
 RN SEQUENCE FROM N.A.
 RP INDUCTION: By phorbol ester (PMA) and lypopolysaccharide (LPS)
 CC treatment in macrophage cell line.
 CC [10].
 RN SEQUENCE FROM N.A.
 RP SIMILARITY: Belongs to the IL-1 family.
 CC -----
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DR EMBL; AF201830; AAF25210.1; -
 DR EMBL; AF186094; AAF0257.1; -
 DR EMBL; AJ242737; CAB59823.1; -
 DR EMBL; AJ242738; CAB59823.1; -
 DR EMBL; AJ271338; CAB67704.1; -
 DR EMBL; AF216693; AAF76981.1; -
 DR EMBL; AF230377; AAF91274.1; -
 DR EMBL; BC024747; AAF24747.1; -
 DR PIR; JCT104; JCT104.
 DR HSSP; P18510; IILR.
 DR Genew; HSCN; 15561; IILF5.
 DR MIM; 605507; -
 DR GO; GO:0005152; F:interleukin-1 receptor antagonist activity; TAS.
 DR InterPro; IPR008996; Cytok_IL1_1like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 DR Cytokine; Multigene family.
 KM SEQUENCE 155 AA; 16962 MW; B96DB5EFA2612E25 CRC64;

Query Match 16.5%; Score 174.5; DB 1; Length 155;
 Best Local Similarity 32.0%; Pred. No. 1,7e-09;
 Matches 54; Conservative 18; Mismatches 48; Indels 49; Gaps 7;

QY 28 NSALCRGPKVKNLNPKKFSLHDDQKVLVDSGNLAVPDKNYIRPIFPALASSLSAS 87
 DB 4 SGALC-----FRKDSALKVLYHNNOL-----LAGLHAGK 35

QY 88 AEKG-----SPILGVSKGFCLYCDKQSGSHSLQKKEKMLK-MAQ 131
 DB 36 VINGEETSVVPMWMLDASLPVILGVGGSGCLSC--GVGQ-EPTLLEPVNIMELYGA 92

QY 132 KESARRPFITRAOVGSMMNLESANHPGFTICSCNCEPVGVTDKREN 180
 DB 93 KES--KSFTEYRDDMGLTSSFSMAYPGWPLCTVPEDQGVRLTQLEPEN 139

RESULT 7
 IIF9_MOUSE STANDARD; PRT; 164 AA.
 ID IIF9_MOUSE
 AC Q9R460;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin 1 family member 9 (IL-1F9).
 GN IL1F9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=21988051; Pubmed=11991723;
 RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;
 RT "Genomic organization of the interleukin-1 locus";
 RL Genomics 79:726-733(2002).
 CC -1- FUNCTION: Function as an agonist of NF-kappa B activation through
 CC the orphan IL-1-receptor-related protein 2. Could constitute part
 CC of an independent signaling system analogous to interleukin-1
 CC alpha (IL-1A), beta (IL-1B) receptor agonist and interleukin-1
 CC receptor type 1 (IL-1RI), that is present in epithelial barriers
 CC and takes part in local inflammatory response (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-1 family.

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DR EMBL; AY071843; AAL67153.1; -
 DR MGD; MGI:2449929; I11f9.
 DR InterPro; IPR008996; Cytok_IL1_1like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
 KM Cytokine; Multigene family.
 SQ SEQUENCE 164 AA; 18733 MW; A7338D475DFEADBE CRC64;

Query Match 16.5%; Score 174.5; DB 1; Length 164;
 Best Local Similarity 31.7%; Pred. No. 1,8e-09;
 Matches 45; Conservative 26; Mismatches 66; Indels 5; Gaps 4;

QY 47 HHDQHKVLVDSGNLAVPDKNYIRPIFPALASSL-SSAAEKGSPILLGVSKGFCL 105
 DB 22 VFLLDQQWVIFRQALVTPRSHRVPTVTLPCXYPESLQDKXIALYILGIONDKCL 81

QY 106 YCDKDKGSHPSLQKKEKMLKAAQKESARRPFITRAOVGSMMNLESANHPGFTICS 165
 DB 82 FCKEVNG--HPTLLKEKILDIYHHP--PMKPFHYHTRGTSTFESVAAPGHYIASS 138

QY 166 CNCNEPVGVTDKFNENKHIIFS 187
 DB 139 KTCN-PIFILTCKGGEYNNINFN 159

RESULT 8
 IIF6_MOUSE STANDARD; PRT; 160 AA.
 ID IIF6_MOUSE
 AC Q9ULR2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Interleukin 1 family member 6 (IL-1F6) (interleukin-1 epsilon) (IL-1
 DE epsilon) (F1L1 epsilon) (interleukin-1 homolog 1) (IL-1H1).
 GN I11F6 OR F11E OR I11E OR I11H1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20209405; Pubmed=10744718;
 RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
 RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
 RA Young P.R.;
 RT "Identification and initial characterization of four novel members of
 RT the interleukin-1 family";
 RL J. Biol. Chem. 275:10308-10314(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21359532; Pubmed=11466363;
 RA Debers R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
 RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
 RA Kastlein R.A.;
 RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
 RT as an antagonist and agonist of NF-kappa B activation through the
 RT orphan IL-1 receptor-related protein 2";
 RL J. Immunol. 167:1440-1446(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shihata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
 RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaletto T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehne H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okita T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boileau D., Bolunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernstein S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima R., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shihata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B.A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- SUBCELLULAR LOCATION: Secreted (potential).
 CC -1- TISSUE SPECIFICITY: Highly expressed in embryonic tissue and in
 CC tissues containing epithelial cells.
 CC -1- MISCELLANEOUS: Binding analysis failed to detect interaction with
 CC multiple IL1R family members.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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 CC -----
 CC EMBL: AF200493; AAF69249.1; -;
 CC EMBL: AF206697; AAG35671.1; -;
 CC EMBL: AK004061; BAB23147.1; -;
 CC HSSP: P01584; 1H1B.
 CC MGD: MGI:1859324; 111f6.
 CC InterPro: IPR008996; Cyclo IL1 like.
 CC InterPro: IPR000975; Interleukin_1.
 CC Pfam: PF00340; IL1; 1.
 CC ProDom: PD002536; Interleukin_1; 1.
 CC SMART: SM00125; IL1; 1.
 CC PROSITE: PS00253; INTERLEUKIN_1; FALSE_NEG.
 CC Cytokine; Multigene family.
 CC KW
 CC SEQUENCE 160 AA; 18015 MW; AA0434D68FF62F4A CRC64;
 Query Match 16.1%; Score 171; DB 1; Length 160;
 Best Local Similarity 31.6%; Pred. No. 3.8e-09;
 Matches 43; Conservative 25; Mismatches 62; Indels 6; Gaps 4;
 Oy 36 KVKNLNPKKFSIHDDHKLVLVDNSGLAVDPKXNYRREIFPAL-ASSLSASAKSPGI 94
 Db 6 ELRAASPELRHVODSSRWLQNNITLAVPKKEGTAVTTTLFCQYLDLTLETNRDPT 65
 Oy 95 LIGVSGKFCFLCYCDKQKQSHPSLQTKKELMKLAQKESARAPRPFRAQVGSWMNES 154
 Db 66 YMGVGRPWSCFLFCTDGEQ-PVQLQSGNIMEMNKKEPKYAS-LFHKXSGTSTRES 122
 Oy 155 AAHPGWF--CTSCNC 168
 Db 123 AAFPGWFVAVCSKSGC 138
 RESULT 9
 IL1X_MOUSE STANDARD; PRT; 178 AA.
 AC P25085; O70207;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IL-1RN)
 GN IL1RN OR IL-1RA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=91250712; PubMed=1828262;
 RA Zahedi K., Seidman M.F., Rits M., Ezeokwiz R.A., Whitehead A.S.;
 RT "Mouse IL-1 receptor antagonist protein. Molecular characterization,
 RT gene mapping, and expression of mRNA in vitro and in vivo.";
 RL J. Immunol. 146:4228-4233(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=91316273; PubMed=1830498;
 RA Matsushima H., Ransel M.F., Matsushima K., Hishinuma A., Sherr C.J.;
 RT "Cloning and expression of murine interleukin-1 receptor antagonist
 RT in macrophages stimulated by colony-stimulating factor 1.";
 RL Blood 78:616-623(1991).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX STRAIN=Swiss;
 MEDLINE=94271931; PubMed=8003626;
 RA Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
 RT "The mouse interleukin 1 receptor antagonist protein: gene structure
 RT and regulation in vitro.";
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX STRAIN=FVB X DBA/1 LACU;
 MEDLINE=98209757; PubMed=9550387;
 RA Gabay C., Porter B., Fantuzzi G., Arend W.P.;
 RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
 RT and protein expression of intracellular isoform and tissue
 RT distribution of secreted and intracellular IL-1 receptor antagonist in
 RT vivo.";
 RL J. Immunol. 159:5905-5913(1997).
 RN [5]
 RP SEQUENCE OF 7-178 FROM N.A.
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
 RA Brandhuber B.J., Thompson R.C.;
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
 RT gene family: evolution of a cytokine control mechanism.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 RN [6]
 RP SEQUENCE OF 23-178 FROM N.A.
 RX MEDLINE=92037824; PubMed=1834470;
 RA Shuck M.E., Eessalu T.E., Tracey D.E., Bienkowski M.J.;
 RT "Cloning, heterologous expression and characterization of murine
 RT interleukin 1 receptor antagonist protein.";
 RL Eur. J. Immunol. 21:2775-2780(1991).
 CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
 CC receptor. Has no IL-1 like activity.
 CC -1- SUBCELLULAR LOCATION: Secreted (isoform 1). Cytoplasmic (isoform
 CC 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P25085-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P25085-2; Sequence=VSP 002652;
 CC -1- SIMILARITY: Belongs to the IL-1 family.
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CC EMBL: W74294; AAA39309.1; -;
 CC EMBL: M64404; AAA39277.1; -;
 DR EMBL: L32838; AAA20576.1; -;
 DR EMBL: AF001795; AAC15251.1; -;
 DR EMBL: M57525; AAA39278.1; -;
 DR EMBL: M61100; AAA39310.1; -;
 DR EMBL: S64082; AAB20265.1; -;
 DR PIR: A44610; A44610.
 DR HSSP: P18510; IIRA.
 DR MGD: MGI:96547; IIRN.
 DR InterPro: IPR008996; Cytok IL1 like.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR ProDom: PD002536; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 26 BY SIMILARITY.
 FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST
 FT DISUPID 92 142 PROTEIN.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT VARSPIC 1 21 N-LINKED (GLCNAC..) (POTENTIAL).
 FT MEICWGYSHLISLLILFPH -> MA (in isoform 2).
 FT /FTID=VSP_002652.
 SQ SEQUENCE 178 AA; 20274 MW; 84AA002A3119C024 CRC64;

Query Match 15.8%; Score 167; DB 1; Length 178;
 Best Local Similarity 31.1%; Pred. No. 1e-08;
 Matches 51; Conservative 26; Mismatches 75; Indels 12; Gaps 7;

QY 28 NSALCGPKKVNLPKKEFSDHDDHKLVLDSCNLIIVDPKXIR-PEIFPALASSLSA 86
 DB 22 SEACRPSGRKPKCKMQAFRIWDTNQKTFYRNQLA---GLQGNI--KLEEKIDMV 75
 QY 87 SAEKSPILIGVSKGEFLCYCDKQSHPSLQKKEKLMKLAQKESARPEIFYRAQV 146
 DB 76 PDLHS-VFGLHGKGLCLSCAKSGDI--KIQLEFVNITDLKKNEDGR-FTFIRSEK 131
 QY 147 GSNMLESAAHPGWFICTSCNCPVGVTDKFNKRHI-EFSFQ 189
 DB 132 GPTTFESAPACPGWFLCTTLEADRPVSLTNTPEEPILVTFYFQ 175

RESULT 10
 IL1A_MOUSE STANDARD; PRT; 152 AA.
 ID IL1A_MOUSE
 AC Q8R459;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin 1 family member 10 (IL-1F10).
 GN IL1F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=21988051; PubMed=11991723;
 RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;
 RT "Genomic organization of the interleukin-1 locus.";
 RL Genome 79:726-733(2002).
 CC -1- FUNCTION: Binds soluble IL-1 receptor type 1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-1 family.
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CC EMBL: AY071844; AAL67155.1; -;
 DR MGD: MGI:2652548; IL1F10.
 DR InterPro: IPR008996; Cytok IL1 like.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR ProDom: PD002536; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; FALSE_NEG.
 KW Cytokine; Multigene family.
 SQ SEQUENCE 152 AA; 17077 MW; 9AD03EB0C3C61D8A CRC64;

Query Match 15.6%; Score 165.5; DB 1; Length 152;
 Best Local Similarity 33.6%; Pred. No. 1.2e-08;
 Matches 49; Conservative 18; Mismatches 72; Indels 7; Gaps 4;

QY 45 FSIHDDHKVLDSCN-LIIVDPKXIRPEIFPALASSLSASAEKSPILIGVSKGEF 103
 DB 10 YIIKDHAQALTYTRNQQLIGDDSDNYSPEKXCILPNGLDRK--VFIFLNGGSGC 66
 QY 104 CYCDKDKQSHPSLQKKEKLMKLAQKESARPEIFYRAQVGSNMLESAAHPGWFIC 163
 DB 67 CLACVXTR--EGFLIQLEDVNIETDLYKGGEQTR-FTFORSIGSAFRIEAAACPGWFLC 123
 QY 164 TSCNCPVGVTDKFNKRHI-EFSFQ 189
 DB 124 GPAEPQAPVQLTKSEPSHTERYFE 149

RESULT 11
 IL1X_HUMAN STANDARD; PRT; 177 AA.
 ID IL1X_HUMAN
 AC P18510; Q14628; Q96GD6; Q9UPC0;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (ICIL-
 DE 1RA) (IRAP) (IL-1RN).
 GN IL1RN OR IL1RA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=90220867; PubMed=2139180;
 RA Carter D.B., Deibel M.R., Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
 RA Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
 RA Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Siew L.C.,
 RA Hardee M.W., Zurcher-Neely H.A., Reardon I.M., Heinikson R.L.,
 RA Truesdell S.E., Shelly J.A., Bessalu T.E., Taylor B.M., Tracey D.E.;
 RT "Purification, cloning, expression and biological characterization of
 RT an interleukin-1 receptor antagonist protein.";
 RL Nature 344:633-638(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=90136921; PubMed=2137201;
 RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
 RA Hannum C.H., Thompson R.C.;
 RT "Primary structure and functional expression from complementary DNA
 RT of a human interleukin-1 receptor antagonist.";
 RL Nature 343:341-346(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
 RA Brandhuber B.J., Thompson R.C.;
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
 RT gene family: evolution of a cytokine control mechanism.";

Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 [4]
 RA SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92338323; PubMed=1385987;
 RA Leonard A., Gorman P., Carrier M., Griffiths S., Scotney H.,
 RA Sheer D., Solari R.;
 RT "Cloning and chromosome mapping of the human interleukin-1 receptor
 RT antagonist gene.";
 RT Cytokine 4:83-89(1992).
 RN [5]
 RA SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 RX MEDLINE=97146044; PubMed=892991;
 RA Jenkins J.K., Diong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
 RA Arend W.P., Smith M.F. Jr.;
 RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
 RT and inducible regulatory regions.";
 RT J. Immunol. 158:748-755(1997).
 RN [6]
 RA SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=91219436; PubMed=1827201;
 RA Haekill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
 RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
 RT "cDNA cloning of an intracellular form of the human interleukin 1
 RT receptor antagonist associated with epithelium.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
 RN [7]
 RA SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=95355865; PubMed=7629520;
 RA Muto M., Polentarutti N., Sironi M., Poli G., De Giola L.,
 RA Introna M., Mantovani A., Colotta F.;
 RT "Cloning and characterization of a new isoform of the interleukin 1
 RT receptor antagonist.";
 RT J. Exp. Med. 182:623-628(1995).
 RN [8]
 RA SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=95172072; PubMed=7867645;
 RA Kleider M.J., Carrington D.P., Haetings N.C., Ahearn M.O.,
 RA Kudanek S.J., Rajkumar N., Toch E.J., Yi Q., Nickerson D.A.;
 RT Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
 RN [9]
 RA SEQUENCE FROM N.A. (ISOFORM 2).
 RX TISSUE=Pancreas;
 RX MEDLINE=23388257; PubMed=12477932;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Datsenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallat D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywnicki M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RA SEQUENCE OF 26-45.
 RX MEDLINE=90136920; PubMed=2137200;
 RA Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,
 RA Heimdel P.L., Ames L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
 RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
 RT inhibitor.";
 RT Nature 343:336-340(1990).
 RN [11]
 RA SEQUENCE OF 26-52.
 RX MEDLINE=90354444; PubMed=2143761;

Bienkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
 RA Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
 RA Heimrickson R.L., Chosay J.G., Tracey D.E.;
 RT "Purification and characterization of interleukin 1 receptor level
 RT antagonist proteins from THP-1 cells.";
 RT J. Biol. Chem. 265:14505-14511(1990).
 RN [12]
 RA SEQUENCE OF 35-177 FROM N.A. (ISOFORM 4).
 RX MEDLINE=98183404; PubMed=9514884;
 RA Weisbach L., Tran K., Colquhoun S.A., Champilaud M.F., Towle C.A.;
 RT "Detection of an interleukin-1 intracellular receptor antagonist mRNA
 RT variant.";
 RT Biochem. Biophys. Res. Commun. 244:91-95(1998).
 RN [13]
 RA STRUCTURE BY NMR.
 RX MEDLINE=92297633; PubMed=1534997;
 RA Stockman B.J., Scallill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
 RA Brunner D.P., Yem A.W., Deibel M.R. Jr.;
 RT "Secondary structure and topology of interleukin-1 receptor
 RT antagonist protein determined by heteronuclear three-dimensional NMR
 RT spectroscopy.";
 RT Biochemistry 31:5237-5244(1992).
 RN [14]
 RA STRUCTURE BY NMR.
 RX MEDLINE=94320651; PubMed=8045306;
 RA Stockman B.J., Scallill T.A., Strakalaitis N.A., Brunner D.P.,
 RA Yem A.W., Deibel M.R. Jr.;
 RT "Solution structure of human interleukin-1 receptor antagonist
 RT protein.";
 RT FEBS Lett. 349:79-83(1994).
 RN [15]
 RA X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94230368; PubMed=8175703;
 RA Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
 RA Brandhuber B.J.;
 RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
 RT resolution.";
 RT J. Biol. Chem. 269:12874-12879(1994).
 RN [16]
 RA X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=95172072; PubMed=7867645;
 RA Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
 RA Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
 RT "Refined crystal structure of the interleukin-1 receptor antagonist.
 RT Presence of a disulfide link and a cis-proline.";
 RT Eur. J. Biochem. 227:838-847(1995).
 RN [17]
 RA X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
 RX MEDLINE=97215904; PubMed=9062194;
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
 RA Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;
 RT "A new cytokine-receptor binding mode revealed by the crystal
 RT structure of the IL-1 receptor with an antagonist.";
 RT Nature 386:194-200(1997).
 RN [18]
 RA -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
 RA receptor. Has no IL-1 like activity.
 CC -1- SUBCELLULAR LOCATION: Secreted (isoform 1). Cytoplasmic (isoforms
 CC 2, 3 and 4).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=P18510-1; Sequence=Displayed;
 CC Name=2; Synonyms=icIL-1ra;
 CC IsoId=P18510-2; Sequence=VSP_002649;
 CC Name=3; Synonyms=icIL-1ra type II;
 CC IsoId=P18510-3; Sequence=VSP_002650;
 CC Name=4;
 CC IsoId=P18510-4; Sequence=VSP_002651;
 CC -1- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
 CC PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -1- DATABASE: NAME=Red Systems' cytokine source book: IL1RN,
 CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=205".

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CC -----
DR EMBL, M5646; AAA59138.1; -
DR EMBL, M6309; AAB41943.1; -
DR EMBL, X52015; CAA36262.1; -
DR EMBL, X53296; CAA37386.1; -
DR EMBL, X64532; CAA45832.1; -
DR EMBL, U65590; AAB92268.1; -
DR EMBL, U65590; AAB92270.1; -
CC -----
Query Match 15.0%; Score 158.5; DB 1; Length 177;
Best Local Similarity 28.7%; Pred. No. 6; Se-08;
Matches 43; Conservative 30; Mismatches 66; Indels 11; Gaps 6;
OY 28 NSALCRGKRVKNLPKRFSDHDDHKVLVDGNIIVADPKNYR-PEIFALASSLSA 86
DB 21 SETICRPGKRSKKQAFRIWDVQKTFYLRNNQLVA-----GYLGPNV--NLEEKIDVV 74
OY 87 SAEKSGPILLGVSKGEFLCYCDKKGSGHPSLQLKKEKLTMLAAKESARRPFIYRAOV 146
DB 75 PIEPFA-FLFIHGKMKLSCVSKSGDER--LQLEAVNITDISENRKODKR-FATIRSDS 130
OY 147 GSWNNLESAHPGMPICTSNCNPEVGYTD 176
DB 131 GPTTSFESAACPGWFLCTAMEADQPVSLTN 160
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RESULT 12
11FA_HUMAN
ID 11FA_HUMAN STANDARD; PRT; 152 AA.
AC Q8MWZ1; Q969H5; Q9BYX1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 family member 10 (IL-1F10) (Interleukin-1 receptor
DE antagonist-like FcIL1 theta (Interleukin-1 theta) (IL-1 theta) (FcIL1
DE theta) (Interleukin-1 HX2) (IL-1HX2) (Interleukin-1 receptor
DE antagonist FKS975).
DE IL1F10 OR FcIL1 OR IL1HX2 OR FKS975.
GN IL1F10 OR FcIL1 OR IL1HX2 OR FKS975.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thymus;
RX MEDLINE=21615180; PubMed=11747621;
RA Bensen J.T., Dawson P.A., Mychaleckyj J.C., Bowden D.W.;
RT "Identification of a novel human cytokine gene in the interleukin gene
RT cluster on chromosome 2q12-14.";
RL J. Interferon Cytokine Res. 21:899-904 (2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Wang Y.-G., Li T., Gong L.;
RT "Identification and characterization of FKS975, a novel member of the
RT interleukin-1 family.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS THR-44 AND ASP-51.
RC TISSUE=fetal skin;
RX MEDLINE=21282953; PubMed=11278614;
RA Lin H., Ho A.-S., Haley-Vicente D., Zhang J., Bernal-Fussell J.,
RA Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
RT "Cloning and characterization of IL1HX2, a novel interleukin-1 family
RT member.";
RL J. Biol. Chem. 276:20597-20602 (2001).

```

[illegible]

DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL1RA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94165101; PubMed=7509813;
RA Cominelli F., Bottolami M., Pizarro T.T., Monsacchi L., Ferretti M.,
RA Brewer M.T., Eisenberg S.P., Ng R.K.;
RT "Rabbit interleukin-1 receptor antagonist. Cloning, expression,
RT functional characterization, and regulation during intestinal
RT inflammation.";
RL J. Biol. Chem. 269:6962-6971(1994).
RN (2)
RP SEQUENCE FROM N.A.
RA Hamada H., Mulligan R.C.;
RL Submitted (XXX-1992) to the EMBL/Genbank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RX MEDLINE=93052512; PubMed=1427977;
RA Goto F., Goto K., Miyata T., Ohkawara S., Takao T., Mori S.,
RA Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.;
RT "Interleukin-1 receptor antagonist in inflammatory exudate cells of
RT rabbits. Production, purification and determination of primary
RT structure.";
RL Immunology 77:235-244(1992).
CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
CC receptor. Has no IL-1 like activity.
CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC -----
DR EMBL: S68977; AAB30093.1; -;
DR EMBL: M57526; AAB31374.1; -;
DR EMBL: D21832; BAA04860.1; -;
DR PIR: A54377; A54377.
DR HSSP: P18510; IL1R.
DR InterPro: IPR008996; Cytok IL1 like.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KM Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 177 BY SIMILARITY.
FT INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 177 AA; 20214 MW; F5BC087F097FEFAF CRC64;
Query Match 14.4%; Score 154.5; DB 1; Length 177;
Best Local Similarity 27.0%; Pred. No. 1.6e-07;
Matches 44; Conservative 23; Mismatches 51; Indels 45; Gaps 6;
QY 32 CRGPKVKNLPKRSIHDOHKVLDLGNLIA-----VDDKNYIRPEI 75
DB 25 CRPGKRCPCRMQARINDVQNKTFYLRNNQVAGYLGCPNAKLEERIDVP---IEPOL 80
QY 76 FPAALSSLSASAEKSPILIGVSKGEFCYCDK--DKGSHPSLQKKEKMLAAQKE 133
DB 81 LF-----LGIGRKLCISCVSGDKMKLH---LEAVNITDLGNKE 118

QY 134 SARPPFIYRAQVGSWMNLESAPHGFICTSCNCEPVGVD 176
DB 119 QDKR-FTFIRNSGPTTFESASCPSWFLCTALADQPVSLTN 160
RESULT 14.
ID IL1X BOVIN STANDARD; PRT: 174 AA.
AC 077482.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IL-1RN)
DE (IRAP).
GN IL1RN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98305607; PubMed=9643454;
RA Kirisawa R., Fukuda T., Yamataka H., Hagiwara K., Goto M., Obata Y.,
RA Yoshino T., Iwai H.;
RT "Enzymatic amplification and expression of bovine interleukin-1
RT receptor antagonist cDNA.";
RL Vet. Immunol. Immunopathol. 62:197-208(1998).
CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
CC receptor. Has no IL-1 like activity.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- SIMILARITY: Belongs to the IL-1 family.
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CC -----
DR EMBL: AB005148; BAA31854.1; -;
DR HSSP: P18510; IL1R.
DR InterPro: IPR008996; Cytok IL1 like.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KM Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 174 BY SIMILARITY.
FT INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 89 139 BY SIMILARITY.
FT CARBOHYD 107 107 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 174 AA; 19926 MW; 1B56E7F224FF851F CRC64;
Query Match 14.4%; Score 152; DB 1; Length 174;
Best Local Similarity 29.6%; Pred. No. 2.6e-07;
Matches 48; Conservative 18; Mismatches 54; Indels 42; Gaps 6;
QY 45 FSIHDOHKVLDLGNLIA-----VDDKNYIRPEIFPALASSLSASA 88
DB 36 FRIVDVQKIFRYLRNNQVAGYLGCPNTKLEKIDVP---IEPHTMF----- 80
QY 89 EKSPILIGVSKGEFCYCDKDGSHPSLQKKEKMLAAQESARPPFIYRAQVGS 148
DB 81 -----LGIHGKLCIACVKSDEI--KLTLEAVNITDLNQNREQDKR-FAFIRFNGP 130
QY 149 WMNLESAPHGFICTSCNCEPVGVD--KFNKRKHIESFQ 189
DB 131 TTSFESAAACPGWFLCTSLADQPVGLINMPTBALKVTKFYFQ 172

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RESULT 15
IL1X CANFA STANDARD; PRT; 176 AA.
ID IL1X CANFA
AC 09BEH0; 09GKK2;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1Ra) (IL-1RN)
DE (IRAP).
GN IL1RN.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin I.-S., Youn H.-Y.;
RT "Molecular cloning of canine interleukin-1 receptor antagonist (IL-1ra)".
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2109092; PubMed=1182158;
RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,
RA Bennett D.;
RT "Cloning of canine IL-1ra, TNFR and TIMP-2."
RL Vet. Immunol. Immunopathol. 78:207-214(2001).
CC -!- FUNCTION: Inhibits the activity of IL-1 by binding to its
CC receptor. Has no IL-1 like activity (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC -----
DR EMBL; AY026462; AAK01472.1; -.
DR EMBL; AF216526; AAG36777.1; -.
DR HSSP; P18510; IL1R.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KM Glycoprotein, signal.
FT FT 1 25 POTENTIAL.
FT CHAIN 26 176 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT FT 91 141 PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 155 155 P -> L (IN REF. 2).
SQ SEQUENCE 176 AA; 13922 MW; 8486CA54A240212B CRC64;

Query Match 14.3%; Score 151; DB 1; Length 176;
Best Local Similarity 28.9%; Pred. No. 3.3e-07;
Matches 46; Conservative 27; Mismatches 76; Indels 10; Gaps 6;

QY 32 CRGPKVKNLNPKKFSIHDDHKLVLDSGNLIVPDKNYIRPELFFALASSLSASAEGK 91
DB 25 CRPLGKRPCRMQAPRIWDVAKTFYLRNQQLVA---GYLQGS-NYKLEKLDVVEPEH 79
QY 92 SPILGVSKGEFCIYCDKDGQSHPSIQLKKEKLMKLAQKESARPPFIYRAQVGSMM 151
DB 80 A-VPLGIHGKTLCLACAKYSGDETR--IQLEAVNITDLSKNKDQKR-FTFILSDSGPTTS 135
QY 152 LESAAHPGFICTSCNCEPEVGVTDKPEKRKH-EPSSFQ 189
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DB 136 FESAACPGWFLCTALEADRPVSLTNRPPEAMWTKYFYQ 174
Search completed: September 9, 2004, 13:25:39
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:20:54 ; Search time 40 Seconds
(without alignments)
488.172 Million cell updates/sec

Title: US-09-869-566-5
1059
Sequence: 1 MSALLILALVGAADVADYKD.....IEFSFQPVCKAEMSPSEVSD 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174.5	16.5	155	2 JC7104	interleukin-1 rece
2	167	15.2	178	2 A44610	interleukin-1 rece
3	161	15.2	180	2 A39386	interleukin-1 rece
4	158.5	15.0	177	2 A30368	interleukin-1 rece
5	154.5	14.6	177	2 A54377	interleukin-1 rece
6	146.5	13.8	178	2 C40956	interleukin-1 rece
7	131.5	12.4	266	2 S23010	interleukin-1 beta
8	128	12.1	267	2 S38373	interleukin-1 beta
9	121.5	11.5	267	1 JN0724	interleukin-1 beta
10	120.5	11.4	269	1 I55969	interleukin-1 beta
11	118	11.1	266	1 ICBO1B	interleukin-1 beta
12	98	9.3	269	1 ICHUB1	interleukin-1 beta
13	95.5	9.0	246	2 B25528	trypsin (EC 3.4.21
14	92.5	8.7	268	2 A30584	interleukin-1 beta
15	91	8.6	404	2 S34031	KTR3 protein - yea
16	89.5	8.5	214	2 JC5646	interleukin-1 beta
17	84	7.9	270	1 ICMS1	interleukin-1 aliph
18	83.5	7.9	776	2 S67053	probable membrane
19	82.5	7.8	246	1 TRRT1	trypsin (EC 3.4.21
20	82	7.7	513	2 T17806	probable flavoprot
21	81	7.6	320	2 A81434	molybdenum cofacto
22	81	7.6	914	2 B96592	hypothetical prote
23	80.5	7.6	246	1 TRRT2	trypsin (EC 3.4.21
24	80.5	7.6	845	2 T17291	hypothetical prote
25	78.5	7.4	244	2 E70224	hypothetical prote
26	78	7.4	1277	2 E70224	hypothetical prote
27	77	7.3	859	2 C67358	hypothetical prote
28	76.5	7.2	231	2 S59589	histone H1 - Chlam
29	76.5	7.2	375	2 F70151	protein-glutamate

30	76.5	7.2	571	2 D86164	hypothetical prote
31	76.5	7.2	627	2 T02846	dynein light chain
32	76	7.2	425	2 T24522	hypothetical prote
33	76	7.2	448	2 JN0118	glucan 1,3-beta-gl
34	75.5	7.1	436	2 AH1387	cell wall binding
35	75	7.1	247	1 TRDG	trypsin (EC 3.4.21
36	75	7.1	247	2 S13813	trypsin (EC 3.4.21
37	75	7.1	247	2 S12764	trypsin (EC 3.4.21
38	75	7.1	314	2 T44311	ADPglyceromanno-he
39	75	7.1	334	2 T34326	homeobox and LIM d
40	74.5	7.0	221	2 F84148	hypothetical prote
41	74.5	7.0	270	1 S10532	interleukin-1 aliph
42	74.5	7.0	504	1 VCPV3A	coat protein - ade
43	74.5	7.0	1116	2 T31432	K-C1 cotransport p
44	74.5	7.0	1199	2 T15826	hypothetical prote
45	74	7.0	728	2 B81370	phosphoribosylform

ALIGNMENTS

RESULT 1
JC7104
Interleukin-1 receptor antagonist - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: JC7104
R:Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, J
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A:Title: IL1H1: A novel interleukin-1 receptor antagonist gene.
A:Reference number: JC7104; MUID:99443727; PMID:10512743
A:Accession: JC7104
A:Molecule type: mRNA
A:Residues: 1-155 <MUI>
A:Cross-references: GB:AF186094; NID:G6049804; PID:AAF02757.1; PID:G6049805
C:Genetics:
A:Gene: il1h1
A:Map position: 2q14
A:Map position: 2q14
C:Keywords: macrophage

Query Match 16.5%; Score 174.5; DB 2; Length 155;
Best Local Similarity 32.0%; Pred. No. 4,7e-09;
Matches 54; Conservative 18; Mismatches 48; Indels 49; Gaps 7;

Qy	28	NSALCRGPKVKNLNPKEFSDHDPKTVLDSCGLAVPDKNYRPRIFFLASLSAS	87
Db	4	SGALC-----FRMKDSALKVLYLNNQL-----LAGLHAGK	35
Qy	88	AEKG-----SPILGVSGEFCLYCDKDGQSHPSLOLKEKLMKL-AAQ	131
Db	36	VIKKEISVVPNRWLDLSLSPVILGVGGSGCLSC--GVGQ-EPTLLEPYNIMELYIGA	92
Qy	132	KESARPFIFPRAQVGSMMLESAAHPGWFICTSCNCPYGVTDKREN	180
Db	93	KES--KSFTFYRDMGLTSSFESAAYPGWFLCTVPEADQPRLTQLPEN	139

RESULT 2
A44610
Interleukin-1 receptor antagonist precursor - mouse
N:Alternate names: IL-1RA
C:Species: Mus musculus (house mouse)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C:Accession: A44610; B40956; A49031; I56106; I52970
R:Matsumine, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sheer, C.J.
Blood 78, 616-623, 1991
A:Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophage
A:Reference number: A44610; MUID:91316273; PMID:1830498
A:Accession: A44610
A:Molecule type: mRNA
A:Residues: 1-178 <MAT>
A:Cross-references: GB:M64404; NID:G198296; PID:AAA39277.1; PID:G198297
R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,

Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
 A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
 A;Reference number: A40956; MUID:91271363; PMID:1828896
 A;Accession: B40956
 A;Molecule type: DNA
 A;Residues: 7-178 <RES>
 A;Cross-references: GB:M63100; NID:g198389; PIDN:AAA9310.1; PID:g198390
 R;Shuck, M.E.; Essalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
 Eur. J. Immunol. 21, 2775-2780, 1991
 A;Title: Cloning, heterologous expression and characterization of murine interleukin 1
 A;Reference number: A49031; MUID:92037824; PMID:1834470
 A;Accession: A49031
 A;Molecule type: mRNA
 A;Residues: 23-178 <SHU>
 A;Cross-references: GB:M74294; NID:g238584; PIDN:AA20265.1; PID:g238585
 A;Experimental source: peritoneal macrophages, ICR strain
 A;Note: Sequence extracted from NCBI Backbone (NCBI:4082, NCBI:64085)
 R;Zahedi, K.; Seidlin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
 J. Immunol. 146, 4228-4233, 1991
 A;Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map
 A;Reference number: I56106; MUID:91250712; PMID:1828262
 A;Accession: I56106
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Cross-references: GB:M74294; NID:g198387; PIDN:AAA9309.1; PID:g198388
 R;Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
 Cytokine 6, 1-9, 1994
 A;Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat
 A;Reference number: I52970; MUID:94271931; PMID:8003626
 A;Accession: I52970
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-178 <RE2>
 A;Cross-references: GB:J32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
 C;Genetics:
 A;Gene: IL-1rn
 A;Intons: 40/2; 70/1; 107/3
 C;Superfamily: interleukin-1
 C;Keywords: cytokine receptor
 F;1-26/Domain: signal sequence #status predicted <SIG>
 F;27-18/Domain: interleukin 1 receptor antagonist #status predicted <MA>
 Query Match 15.8%; Score 167; DB 2; Length 178;
 Best Local Similarity 31.1%; Pred. No. 2.8e-08;
 Matches 51; Conservative 26; Mismatches 75; Indels 12; Gaps 7;
 QY 28 NSALCRGPVKYNLPKFFSIHDDHKLVLDSGNLIVDPKNYIR-DEIFPALASSLSA 86
 Db 22 SEAACRPSGRKPCMQAFRIWDTNQTFYLRNQLIA---GYLQGNII--KLEEKIDMV 75
 QY 87 SAEKGSPIILGVSGEFCYCDKDKGSHSLQKKRKLAAQKSARRPFIFYAQV 146
 Db 76 PIDLHS-VFPIGHGKCLCLCAKSGDDI--KLQEEVNIIDLSKNKEDKR-FTPIRSEK 131
 QY 147 GSNMMLSAHPGWFICTSCNCPVGVTDKFEKRII-EFSFQ 189
 Db 132 GPITTSFSAACPGWFLCTTLEADPFVSLINPEPPLIVTYFYFO 175
 RESULT 3
 A39386
 Interleukin-1 receptor antagonist, long intracellular splice form - human
 N;Contains: Interleukin-1 receptor antagonist, short intracellular splice form
 C;Species: Homo sapiens (man)
 C;Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
 C;Accession: I37893; A39386
 R;Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovani
 J. Exp. Med. 182, 623-628, 1995
 A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
 A;Reference number: I37893; MUID:95355865; PMID:7629520
 A;Accession: I37893
 A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA
 A;Residues: 1-180 <RES>
 A;Cross-references: EMBL:X84348; NID:g1008970; PIDN:CAA59087.1; PID:g1008971
 R;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.T.;
 Proc. Natl. Acad. Sci. U.S.A. 88, 3691-3695, 1991
 A;Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor antag
 A;Reference number: A39386; MUID:91219436; PMID:1827201
 A;Accession: A39386
 A;Molecule type: mRNA
 A;Residues: 1-3, 25-180 <HMS>
 A;Cross-references: GB:M55646; NID:g186291; PIDN:AA59138.1; PID:g186292
 C;Comment: For an alternative splice form, see PIR:A30368
 C;Genetics:
 A;Gene: GDB:IL1RN
 A;Cross-references: GDB:125897; OMIM:147679
 A;Map position: 2q14.2-q14.2
 C;Superfamily: interleukin-1
 C;Keywords: alternative splicing; cytokine receptor
 F;1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form
 F;1-3, 25-180/Product: interleukin-1 receptor antagonist, short intracellular splice form
 Query Match 15.2%; Score 161; DB 2; Length 180;
 Best Local Similarity 27.9%; Pred. No. 1e-07;
 Matches 48; Conservative 35; Mismatches 71; Indels 18; Gaps 8;
 QY 13 AVAD-YKD-----DDKTLAANSALCRGPVKYNLPKFFSIHDDHKLVLDSGNLIV 65
 Db 2 ALADLYEBGGGGGGBEDNADSKETICRPSGRSSKQAFRIWDVQKTFYLRNQLVA- 60
 QY 66 PDKNYIR-DEIFPALASSLSASAEKSPILLGVSGEFCYCDKDKGSHSLQKKR 124
 Db 61 ---GYLQGNIV--NLEEKIDVPIEHPA-LFLGIGHGKXCLSCVKSDETR--LQLEAVN 112
 QY 125 LKTLAAQKSARRPFIFYAQVGSNMMLSAHPGWFICTSCNCPVGVTD 176
 Db 113 ITDLSNRKQDKR-FAPIRSDSGPTTSFSAACPGWFLCTTLEADQPVSLTN 163
 RESULT 4
 A30368
 Interleukin-1 receptor antagonist secreted form precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000
 C;Accession: A40956; MUID:917894; A30368; S08160; S08159; A37822
 R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
 Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
 A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
 A;Reference number: A40956; MUID:91271363; PMID:1828896
 A;Accession: A40956
 A;Molecule type: DNA
 A;Residues: 1-177 <RES>
 A;Cross-references: GB:M63109; NID:g186385; PIDN:AA61943.1; PID:g186386
 R;Lemard, A.; Gorman, P.; Carriere, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari, R.
 Cytokine 4, 83-89, 1992
 A;Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist ge
 A;Reference number: I37894; MUID:92338323; PMID:1385887
 A;Accession: I37894
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-177 <LEN>
 A;Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
 R;Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slichtom, J.
 J.G.; Siu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; Tr
 Nature 344, 633-638, 1990
 A;Title: Purification, cloning, expression and biological characterization of an interl
 A;Reference number: A30368; MUID:90220867; PMID:2139180
 A;Accession: A30368
 A;Molecule type: mRNA
 A;Residues: 1-177 <CAR>
 A;Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
 A;Note: parts of this sequence, including the amino end of the mature protein, were confi
 R;Eisenberg, S.P.; Evans, R.U.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.; J
 Nature 343, 341-346, 1990

A/Title: Primary structure and functional expression from complementary DNA of a human
A/Reference number: S08160; MUID:90136921; PMID:2137201
A/Accession: S08160
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-177 <E12>
A/Cross-references: GB:X52015; NID:932576; PIDN:CA56262.1; PID:932577
R:Hannun, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Driggs, D.J.; Heimdal, P.L.; At
Nature 343, 336-340, 1990
A/Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.
A/Reference number: S08159; MUID:90136920; PMID:2137200
A/Accession: S08159
A/Molecule type: protein
A/Residues: 26-75; 97-108; 110-116; 120-131; 163-176 <HAN>
R:Bienkowski, M.U.; Bessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde,
J. Biol. Chem. 265, 14505-14511, 1990
A/Title: Purification and characterization of interleukin 1 receptor level antagonist pr
A/Reference number: A37822; MUID:90354444; PMID:2143761
A/Accession: A37822
A/Molecule type: protein
A/Residues: 26-52; 70-77; 122-127; 170-175 <BIE>
A/Experimental source: culture medium, PMA-stimulated THP-1 cells
A/Comment: For an alternative splice form, see PIR:A39386
C/Genetics:
A/Gene: GDB:IL1RN
A/Cross-references: GDB:125897; OMIM:147679
A/Map position: 2q14.2-2q14.2
A/Intons: 39/2; 69/1; 106/3
C/Superfamily: interleukin-1
C/Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:129/Product: interleukin-1 receptor antagonist #status experimental <MAT>
F:109/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 15.0%; Score 158.5; DB 2; Length 177;
Best Local Similarity 28.7%; Pred. No. 1.8e-07;
Matches 43; Conservative 30; Mismatches 66; Indels 11; Gaps 6;
Qy 28 NSALCRGPKVKNLPKRSIHDOHKVLVLDGSLIAPDKNYR-PIPIFALSSLSA 86
Db 21 SETICRPSGRKSSKQAFRIWDVQKTFYLRNNQLVA---GYLQGPVNV--NLEEKIDIV 74
Qy 87 SAEKSPILIGVSGEPLCYCDKXGSHPSLOLKKKELMTLAQKESARPPFIYRAQV 146
Db 75 PIEPHA-LFGIHGKCKLSCVSKSGDEIR--LQLEAVNITDLSNRKDKR-FAPIRSDS 130
Qy 147 GSMNMLSAHPGWFICTSCNCPNPGVTD 176
Db 131 GPTTSPESAACPGWFLCTAMADQPVSLTN 160
RESULT 5
A54377
interleukin-1 receptor antagonist secreted form precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C/Accession: A54377; 146729
R:Cominelli, F.; Borcolami, M.; Piarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T.
J. Biol. Chem. 269, 6962-6971, 1994
A/Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional char
A/Reference number: A54377; MUID:94165101; PMID:7509813
A/Accession: A54377
A/Molecule type: mRNA
A/Residues: 1-177 <COM>
A/Cross-references: GB:S68977; NID:9545740; PIDN:AA30093.1; PID:9545741
A/Experimental source: colon tissue
A/Note: sequence extracted from NCHI backbone (NCBIN:14168, NCBI:P:144169)
R:Goto, F.; Goto, K.; Miyata, T.; Okawara, S.; Takeo, T.; Mori, S.; Furukawa, S.; Maeda
Immunology 77, 235-244, 1992
A/Title: Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. Pro
A/Reference number: 146729; MUID:93052512; PMID:1427977
A/Accession: 146729
A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-177 <GOT>
A/Cross-references: GB:D21832; NID:9425787; PIDN:BA04860.1; PID:9425205
C/Superfamily: interleukin-1
C/Keywords: cytokine receptor; extracellular protein; glycoprotein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:109/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.6%; Score 154.5; DB 2; Length 177;
Best Local Similarity 27.0%; Pred. No. 4.2e-07;
Matches 44; Conservative 23; Mismatches 51; Indels 45; Gaps 6;
Qy 32 CRGPKVKNLPKRSIHDOHKVLVLDGSLIAPDKNYR-PIPIFALSSLSA 86
Db 25 CRGPKVKNLPKRSIHDOHKVLVLDGSLIAPDKNYR-PIPIFALSSLSA 86
Qy 76 FFALASSLSASAEKSPILIGVSGEPLCYCDKXGSHPSLOLKKKELMTLAQK 133
Db 81 LF-----LGIRGKLCISCVSGDKMKH-----LEAVNITDLSNRK 118
Qy 134 SARPPFIYRAQVGSMMNMLSAHPGWFICTSCNCPNPGVTD 176
Db 119 QDKR-FTFIRNSGPTTTFESASCPGWFLCTALADQPVSLTN 160
RESULT 6
A40956
interleukin-1 receptor antagonist precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C/Accession: A40956
R:Bienberg, S.P.; Brewer, M.T.; Verdier, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5235-5236, 1991
A/Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A/Reference number: A40956; MUID:91271363; PMID:1828896
A/Accession: A40956
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-178 <E15>
A/Cross-references: GB:M63101; NID:9204928; PIDN:AAA41434.1; PID:9204929
C/Superfamily: interleukin-1
C/Keywords: cytokine receptor
Query Match 13.8%; Score 146.5; DB 2; Length 178;
Best Local Similarity 26.6%; Pred. No. 2.4e-06;
Matches 47; Conservative 23; Mismatches 58; Indels 49; Gaps 6;
Qy 31 LCRGPKVKNLPKRSIHDOHKVLVLDGSLIAPDKNYR-PIPIFALSSLSA 86
Db 3 ICRGPKVKNLPKRSIHDOHKVLVLDGSLIAPDKNYR-PIPIFALSSLSA 86
Qy 65 ----VDPKNIYRPIPIFALSSLSASAEKSPILIGVSGEPLCYCDKXGSHPSLO 119
Db 63 GPNTKLEKIDWVIDP-----RNVPFGIHGKCKLSCVSKSGDDT--KLQ 105
Qy 120 LKKEKMTLAQKESARPPFIYRAQVGSMMNMLSAHPGWFICTSCNCPNPGVTD 176
Db 106 LEEVNTDLMNKKEDKR-FTFIRNSGPTTTFESASCPGWFLCTALADQPVSLTN 161
RESULT 7
S23010
interleukin-1 beta precursor - sheep
N/Alternate names: hematopoietin-1; IL-1 beta
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
C/Accession: S23010; S43047; S133092; B61246
R:Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A/Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A/Reference number: S23010; MUID:92119335; PMID:1840515
A/Accession: S23010
A/Molecule type: mRNA

A/Residues: 1-266 <SEO>

A/Cross-references: EMBL:X56972; NID:G1808; PIDN:CAA40293.1; PID:G1809

A/Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an additional R/Sargan, D.R. submitted to the EMBL Data Library, May 1992

A/Reference number: S43047

A/Accession: S43047

A/Molecule type: mRNA

A/Residues: 1-113, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <SAR>

A/Cross-references: EMBL:X54796; NID:G1273; PIDN:CAA38566.1; PID:G1274

R/Fiskersrud, C.; Sargan, D.

Nucleic Acids Res. 18, 7165, 1990

A/Title: Nucleotide sequence of ovine interleukin-1 beta.

A/Reference number: S13092; MUID:91088326; PMID:2263490

A/Accession: S13092

A/Molecule type: mRNA

A/Residues: 1-113, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <FTS>

A/Cross-references: EMBL:X54796

A/Note: the authors translated the codon AGT for residue 62 as Arg

R/Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.

Immunology 74, 453-460, 1991

A/Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.

A/Reference number: A61246; MUID:92120716; PMID:1769692

A/Accession: B61246

A/Molecule type: mRNA

A/Residues: 1-144, 'L', 146-266 <AND>

C/Comment: This protein lacks a conventional signal sequence for protein export. Cleaved form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.

C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a

C/Genetics:

A/Gene: IL-1-beta

C/Superfamily: Interleukin-1

C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen

F,114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 12.4%; Score 131.5; DB 1; Length 266;

Best Local Similarity 27.2%; Pred. No. 9,7e-05;

Matches 44; Conservative 30; Mismatches 63; Indels 25; Gaps 8;

QY 17 YKDDDKL---AAANSALCRGPKVKNLPPKFSIHODHVLVLDG---NLIAVPDKNY 70

Db 103 FETSSBELLDAAVQSVKCK-----LDREQKSLVLDSPCVKALHLPSQEM 149

QY 71 IRPEIFALASSLSASAEKSPILLVGSKGEFLCYDKQKQSHPSLQKKEKMLGLAA 130

Db 150 SR-EVVFPCW-SFVQGERDKKIFVALGIRDKNLYLSCVK-KGDT-PTLQ--EVDPKVY 203

QY 131 QKESARRPFIYRAOVGSNNMLESAAHPGFICTSCNCEPV 172

Db 204 PKNMEKRFVFKTEIKNTEVFESVLYPNWYISTQAEKPV 245

RESULT 8

S38373

Interleukin-1 beta precursor - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999

R/Vandendriock, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde

Eur. J. Biochem. 217, 45-52, 1993

A/Title: Gene sequence, cDNA construction, expression in *Escherichia coli* and geneticall

A/Reference number: S38373; MUID:94039070; PMID:8223564

A/Accession: S38373

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-267 <VAN>

A/Cross-references: EMBL:X74568; NID:9407899; PIDN:CAA52660.1; PID:9407900

C/Genetics:

A/Insertions: 16/2; 33/3; 99/1; 154/1; 197/3

C/Superfamily: Interleukin-1

Query Match 12.1%; Score 128; DB 2; Length 267;

Best Local Similarity 28.9%; Pred. No. 0.00021;

Matches 43; Conservative 28; Mismatches 66; Indels 12; Gaps 6;

QY 27 ANSALCRGPKVKNLPPKFSIHODHVLVLDGSLIAVPD--KNYIRPEIFALASSLS 84

Db 107 ANGFLDAPVQSVQDK---LDQDEKALVLAGPHLKLHLKGLKREVFCHSFGVG 163

QY 85 SASAEKSPILLVGSKGEFLCYC-DKQKQSHPSLQKKEKMLAAQESARRPFIYR 143

Db 164 DQSDDK-IVTLGIGKKNLYLSCVMKD---DPTLQ--EDVDPKSYPRDKMEKRFVFK 217

QY 144 AOVGSNNMLESAAHPGFICTSCNCEPV 172

Db 218 TEIKNVEFESALYPNWYISTQAEQKPV 246

RESULT 9

JN0724

Interleukin-1 beta precursor - pig

N/Alternate names: hematopoietin-1; IL-1 beta

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999

C/Accession: JN0724

R/Huetter, M.J.; Lin, G.; Smith, D.M.; Murrugh, M.P.; Mollitor, T.W.

Gene 129, 285-289, 1993

A/Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 bet

A/Reference number: JN0724; MUID:93314975; PMID:8325511

A/Accession: JN0724

A/Molecule type: mRNA

A/Residues: 1-267 <HUE>

A/Cross-references: GB:M86725; NID:G164607; PIDN:AAA02584.1; PID:G164608

A/Experimental source: alveolar macrophage

C/Comment: This protein is a pleiotropic cytokine that mediates a variety of processes in

C/Comment: This protein lacks a conventional signal sequence for protein export. Cleavage

ved form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.

C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a

C/Superfamily: Interleukin-1

C/Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage

F,115-267/Product: interleukin-1 beta #status predicted <LIL>

F,77/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 11.5%; Score 121.5; DB 1; Length 267;

Best Local Similarity 25.9%; Pred. No. 0.00084;

Matches 44; Conservative 28; Mismatches 73; Indels 25; Gaps 7;

QY 19 DDDDK-----LAANSALCRGPKVKNLPPKFSIHODHVLVLDGSLIAV 65

Db 86 DDDQKSIFFIFEEPIILETCNDPVCDAVQSECK---LDQKQKSLVLAGPHLKA 142

QY 66 PD--KNYIRPEIFALASSLSASAEKSPILLVGSKGEFLCYC-DKQKQSHPSLQK 122

Db 143 LHLTGDLKREVFCH-SFVQGDSDSNKKTPTVLGIGKKNLYLSCVMKD---NPTLQ-- 196

QY 123 EKIMKLAQKESARRPFIYRAOVGSNNMLESAAHPGFICTSCNCEPV 172

Db 197 EDIDPKRYPRDKMEKRFVFKTEIKNVEFESALYPNWYISTQAEQKPV 246

RESULT 10

I55969

Interleukin-1 beta precursor - mouse

N/Alternate names: hematopoietin-1; IL-1 beta

C/Species: Mus musculus (house mouse)

C/Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999

C/Accession: I55969; A24719; S13029

R/Gray, P.W.; Gaisster, D.; Chen, E.; Goedel, D.V.; Pennica, D.

J. Immunol. 137, 3644-3648, 1986

A/Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for mu

A/Reference number: I55969; MUID:87058957; PMID:3491144

A/Accession: I55969

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-269 <RES>

A/Cross-references: GB:M15131; NID:G198293; PIDN:AAA9276.1; PID:G309398

A:Title: The murine interleukin-1-beta gene: structure and evolution.
A:Reference number: A24719, MUID:87117546, PMID:3492706
A:Accession: A24719
A:Molecule type: mRNA
A:Residues: 1-269 <TEL>
A:Cross-references: GB:X04964; NID:G52666; PIDN:CAA28637.1; PID:G52667
R:Damuy, G.O.; Wilder, C.L.; Merenda, J.M.; Mccoll, A.S.; Geoghegan, K.F.; O'ternness, I
FEBS Lett. 278, 98-102, 1991
A:Title: Reduction of biological activity of murine recombinant interleukin-1beta by se
A:Reference number: S13029, MUID:91130610, PMID:1993481
A:Accession: S13029
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 118-269 <DAU>
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleava
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C:Genetics:
A:Gene: IL-1-beta
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F:118-269/Product: interleukin-1 beta #status experimental <Ill>

Query Match	11.4%	Score 120.5	DB 1	Length 269
Best Local Similarity	27.8%	Pred No. 0.0011		
Matches	50	Conservative	34	Mismatches 79, Indels 17, Gaps 9
Qy	14	VADYKDDDDKLAANSALCRGPVKNLANKPKESIHDDHKVLT-DSGNLIAPV-DKNTYI	71	
Db	103	LCDSMDDDD-----NLVGCDFP-IRQLH---YRLRGEQKSLVLSDFELKALHLNGQNI	153	
Qy	72	RPEIFPALASSLSASAEKGSPTLLGSKGEFCLYCDKDGQSHPSLDLKKETKMLKLAQ	131	
Db	154	NOQVIFSSMSFVQGEPSNDK-IPVALGLKKKNLYLSCVMMDGT--PTQLQ--ESVDPKQYP	208	
Qy	132	KESARPRFLFYAAQVGSMMMLSSAARHGMFICTSCNCPNRYGTIDFKENRKHIEFSQPV	191	
Db	209	KKGEKREKVENKIEVKSKEVFEPSAERPNMYIISTSQAEHKPVFLGNN-SGGDIIIDFTMEISV	267	

RESULT 11

interleukin-1 beta precursor - bovine
N:Alternate names: hematopoietin-1, IL-1 beta
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C:Accession: J10010, S01380
R:Matizawasi, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S., et al.
Mol. Immunol. 25, 429-437, 1988
A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin
A:Reference number: A94695; MUID:88318652; PMID:3261832
A:Accession: J10010
A:Molecule type: mRNA
A:Residues: 1-266 <MAL>
A:Cross-references: GB:M77211; NID:G163200; PIDN:AAA30584.1; PID:G163201
R:Leong, S.R.; Flagg, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A:Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
A:Reference number: S01380; MUID:89016591; PMID:3262866
A:Accession: S01380
A:Molecule type: mRNA
A:Residues: 1-251, 'A', 253-266 <LEO>
A:Cross-references: EMBL:X12498; NID:G448; PIDN:CAA31018.1; PID:G449
C:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and in-
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavag-
ved form of interleukin-beta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-beta precursor is less heavily myristoylated than interleukin-lactat-
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
P:114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 11.1%; Score 118; DB 1; Length 266;
 Best Local Similarity 25.4%; Pred. No. 0.0018;
 Matches 46; Conservative 33; Mismatches 76; Indels 26; Gaps 8

```

QY      9 LVGAADVADYKDDDDKLA-----AANSALCRGPVKYNLPKPKFSIHDQHK 53
DB      74 LRNAAYAVHFDDDDLRSLISLFIPEEHPVIFETSSDEFLCDAP--VQSI---KCKLDDREOK 129
QY      54 VLVADSGNLIAMPD--KNYIRPEIFPALASSLSASMAEKGAPILLGVGSKGEFCIYCDKDX 111
DB      130 SLVLASPCVLAALHLHLSQEMNREVVEFCM--STVQGERPNKIKPALGIDKXILYSCKV-K 187
QY      112 GQSHPSIQLKTEKLTMLAOKESAARRPFIYRAQGVSNMLESAAHPGMWICTSCNCEP 171
DB      188 GDT--PTIQL--EEVDPKYVPRKRNMEKREVFVKTETIKNTVEESVLVPMWYISTSIQIEEP 244
QY      172 V 172
DB      245 V 245

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RESULT 12

Interleukin-1 beta precursor [validated] - human
N.Alternate names: hematopoietin-1; IL-1 beta
C.Species: Homo sapiens (man)
C.Date: 28-Feb-1986 #sequence, revision 15-May-1998 #text, change 15-Sep-2000
C.Accession: A25542; A29019; A94023; A93361; I51852; I65500; I39132; B27616; A01848; S19
R.Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Atron, P.E.
Nucleic Acids Res. 14, 7897-7914, 1986
A.Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev
A.Reference number: A25542; MUID:87040762; PMID:3490654
A.Accession: A23542
A.Molecule type: DNA; mRNA
A.Residues: 1-5, 'K', 7-269 <CLA>
A.Cross-references: GB:X04500; NID:g33788
A.Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu
R.Bensi, G.; Raugi, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.
Gene 52, 95-101, 1987
A.Title: Human interleukin-1 beta gene.
A.Reference number: A29019; MUID:87248099; PMID:2954882
A.Accession: A29019
A.Molecule type: DNA
A.Residues: 1-269 <BEN>
A.Cross-references: GB:M15640; NID:g186281; PIDN:AAA74137.1; PID:g386816
R.Auton, P.E.; Webb, A.C.; Rosenwasser, L.U.; Mucci, S.F.; Rich, A.; Wolfe, S.M.; Dinarello
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A.Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A.Reference number: A94023; MUID:85088517; PMID:6083565
A.Accession: A94023
A.Molecule type: mRNA
A.Residues: 1-5, 'K', 7-269 <AUR>
A.Cross-references: GB:X02770; NID:g186268; PIDN:AAA36106.1; PID:g307403
R.March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.
Nature 315, 641-647, 1985
A.Title: Cloning, sequence and expression of two distinct human interleukin-1 complement
A.Reference number: A93361; MUID:85240547; PMID:2289698
A.Accession: A93361
A.Molecule type: mRNA
A.Residues: 1-269 <MB>
A.Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790
A.Note: Parts of this sequence, including the amino end of the mature form, were confirm
R.Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolfe, S.M.; Au
Adv. Gene Technol. 22, 339-340, 1985
A.Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A.Reference number: I51852
A.Accession: I51852
A.Status: translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MB>
A.Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1; PID:g186288
R.Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; Hira
Biochem. Biophys. Res. Commun. 143, 345-352, 1987

A:Residues: 1-268 <CAN>
A:Cross-references: GB:M6295; NID:9516632; PIDN:AAA31373.1; PID:9516633
R:Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A:Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and
A:Reference number: A94230; MUID:89315718; PMID:287507
A:Accession: J00082
A:Molecule type: mRNA
A:Residues: 1-268 <YOU>
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
ved form of interleukin-1 beta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-1 beta precursor is less heavily myristoylated than interleukin-1
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F:117-268/Product: interleukin-1 beta #status predicted <IIB>

Query Match 8.7%; Score 92.5; DB 1; Length 268;
Best Local Similarity 24.7%; Pred. No. 0.44;
Matches 44; Conservative 26; Mismatches 81; Indels 27; Gaps 7;

Qy 16 DYKDDDKLAANALCGPKVKNLPKPSIHQDHVLYDSGNLIAVPDKN--YIRP 73
Db 110 DYSLECD---AVRSIHCR-----LQDAQKSLVLSGYELKALHINAEINQ 153
Qy 74 EIPFALASSLSASAEKSGSPILLGVSKGEFCLYC--DKDKGSHPSLQKKKXMKLAQ 131
Db 154 QVFSMSVTVQGESNDK-IPVALGLRGKLYLSCVMKDK---PTLQL--ESVDPNRY 206

Qy 132 KESARPFIFYRAQVGSNMLESAAHPGMFICTSCNCPVGVTDKFNKRKHIEFSFQ 189
Db 207 KKKMEKRVFVKIEIKDLFEPSAQFPWYISTSGTEYMPFLGNNSGQDLIDPSME 264

RESULT 15
S34031
KTR3 protein - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YBR145; protein YBR205W
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: S34031; S46077; S34928
R:Jacquet, M.
submitted to the EMBL Data Library, January 1993
A:Reference number: S34022
A:Accession: S34031
A:Molecule type: DNA
A:Residues: 1-404 <JAC>
A:Cross-references: EMBL:Z21487; NID:9311665; PID:9311682
R:Busseau, F.; Demolis, N.; Jacquet, M.; Maillet, L.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S46054
A:Accession: S46077
A:Molecule type: DNA
A:Residues: 1-404 <BUS>
A:Cross-references: EMBL:Z36074; NID:9536582; PID:9536583; MIPS:YBR205W
R:Busseau, F.; Maillet, L.; Gallion, L.; Jacquet, M.
Yeast 9, 797-806, 1993
A:Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome II
A:Reference number: S34925; MUID:93377417; PMID:8368014
A:Accession: S34928
A:Molecule type: DNA
A:Residues: 91-352 <BU2>
A:Cross-references: EMBL:Z21487
C:Genetics:
A:Gene: SGD:KTR3
A:Cross-references: SGD:S0000409; MIPS:YBR205W
A:Map position: 2R
C:Keywords: transmembrane protein
F:22-45/Domain: transmembrane #status predicted <TM>

Query Match 8.6%; Score 91; DB 2; Length 404;
Best Local Similarity 22.8%; Pred. No. 0.99;
Matches 36; Conservative 20; Mismatches 58; Indels 44; Gaps 5;

Qy 46 SIHQDHVLYDSGNLIAVPDKNYIRPE-----IPFALASSLSASAEKSGPIL 95
Db 2 SVH---HKKLMPSALIRKYQGISSFFGLIIVLSFLFMGSRSPVPIAQTISVS 58
Qy 96 LGVSKGEFCLYCDKDKGSHPSLQKKKXMKLAOKESARPFIFYRAQVGSNMLES 155
Db 59 RVASKDYLPPTDKSGVYHFPVDQKKEKGVMTLARS-----DLNVLVXSI 106
Qy 156 AHPGMFICTSCNCPVGVTDKFNKRKHIEFSF---QP 190
Db 107 RH-----VEDRFNNRYHYDVPFLNDQP 128

Search completed: September 9, 2004, 13:28:28
Job time : 42 secs

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